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OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 23:21:40 ; Search time 312 Seconds  
(without alignments)  
3483.830 Million cell updates/sec

Title: US-10-824-981-1  
Perfect score: 1343  
Sequence: 1 CTCGAGGATCTGCGGCGG.....atacccttaaatgaggtacc 1343

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330.8	99.1	2755	8	US-11-000-688-73
2	205.6	15.3	269	8	Sequence 73, Appl
3	204.2	15.2	472	8	Sequence 72, Appl
4	204.2	15.2	472	8	Sequence 2285, Ap
5	53.4	4.0	387	8	Sequence 5927, Ap
6	40.8	3.0	598	7	Sequence 71, Appl
7	40.8	3.0	598	7	Sequence 21506, A
8	39.6	2.9	1236	7	Sequence 21506, A
9	39.6	2.9	1236	7	Sequence 59374, A
10	39.4	2.9	1542	7	Sequence 59374, A
11	39.4	2.9	1542	7	Sequence 51728, A
12	39.4	2.9	1659	7	Sequence 47, Appl
13	39.4	2.9	4419	7	Sequence 51728, A
14	39.4	2.9	4419	7	Sequence 25730, A
15	38.8	2.9	191331	8	Sequence 25730, A
16	38.6	2.9	1519	7	Sequence 20, Appl
17	38.6	2.9	1519	7	Sequence 46824, A
18	38.6	2.9	1959	8	Sequence 46824, A
19	38.4	2.9	172649	8	Sequence 3, Appl
20	37.8	2.8	21142	7	Sequence 36, Appl
21	37.6	2.8	3001	8	Sequence 13380, A
22	37.4	2.8	5562	7	Sequence 178, App
					Sequence 63, Appl

23	37	2.8	83528	7	US-10-995-561-13343	Sequence 13343, A
24	37	2.8	1080000	7	US-10-928-446A-1	Sequence 1, Appli
25	37	2.8	1080000	7	US-10-928-446A-181	Sequence 181, App
26	37	2.8	1080000	7	US-10-928-446A-183	Sequence 183, App
27	37	2.8	1080000	7	US-10-928-446A-185	Sequence 185, App
28	37	2.8	1080000	7	US-10-928-446A-187	Sequence 187, App
29	37	2.8	1080000	7	US-10-928-446A-189	Sequence 189, App
30	37	2.8	1080000	7	US-10-928-446A-191	Sequence 191, App
31	37	2.8	1080000	7	US-10-928-446A-193	Sequence 193, App
32	37	2.8	1080000	7	US-10-928-446A-195	Sequence 195, App
33	37	2.8	1080000	7	US-10-928-446A-197	Sequence 197, App
34	37	2.8	1080000	7	US-10-928-446A-199	Sequence 199, App
35	37	2.8	1080000	7	US-10-928-446A-201	Sequence 201, App
36	36.8	2.7	600	7	US-10-750-185-756	Sequence 756, App
37	36.8	2.7	600	7	US-10-750-623-756	Sequence 756, App
38	36.8	2.7	918	7	US-10-750-185-38838	Sequence 38838, A
39	36.8	2.7	918	7	US-10-750-623-38838	Sequence 38838, A
40	36.4	2.7	764	7	US-10-750-185-59751	Sequence 59751, A
41	36.4	2.7	764	7	US-10-750-623-59751	Sequence 59751, A
42	36.4	2.7	1685	7	US-10-750-185-29078	Sequence 29078, A
43	36.4	2.7	1685	7	US-10-750-623-29078	Sequence 29078, A
44	36.4	2.7	1994	7	US-10-750-185-26833	Sequence 26833, A
45	36.4	2.7	1994	7	US-10-750-623-26833	Sequence 26833, A

ALIGNMENTS

RESULT 1  
US-11-000-688-73  
; Sequence 73, Application US/11000688  
; Publication No. US20050287544A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, Francois  
; APPLICANT: HOULGATTE, Remi  
; APPLICANT: BIRNBAUM, Daniel  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS  
; FILE REFERENCE: 1423-R-03  
; CURRENT APPLICATION NUMBER: US/11/000,688  
; PRIOR FILING DATE: 2004-12-01  
; PRIOR APPLICATION NUMBER: US 60/525,987  
; PRIOR FILING DATE: 2003-12-01  
; NUMBER OF SEQ ID NOS: 1596  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 73  
; LENGTH: 2755  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial sequences:primer  
; NAME/KEY: misc feature  
; LOCATION: (1)..(2755)  
; OTHER INFORMATION: Interferon (alpha, beta and omega) receptor  
; OTHER INFORMATION: 1(IFNARI) gene.  
US-11-000-688-73

Query Match	99.1%;	Score 1330.8;	DB 8;	Length 2755;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1332;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;
Qy	1	CTGCAGGATCTGCGGCGGCTCCAGATGATGGTCTCTCTGCGCGCGACGACCTAG	60	
Db	53	CTGTGGGATCTGCGGCGGCTCCAGATGATGGTCTCTCTCTGCGCGCGACGACCTAG	112	
Qy	61	TGCTGTGCGCGTGGGCGGCTAGGTTGTTCGCGCGCGAGGTGGAAAAAATCTAAAT	120	
Db	113	TGCTGTGCGCGTGGGCGGCTAGGTTGTTCGCGCGCGAGGTGGAAAAAATCTAAAT	172	
Qy	121	CTCTCAAAAAGTAGAGTTCACATCATAGTACAACTTTATCTGAGGTGGACAGGA	180	
Db	173	CTCTCAAAAAGTAGAGTTCACATCATAGTACAACTTTATCTGAGGTGGACAGGA	232	

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QY 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGATA 240
Db 233 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGATA 292
QY 241 ATTGGATAAAATGCTCTGGGTGTGAGATATTACTAGTACCAATGCAATTTCTTCAC 300
Db 293 ATTGGATAAAATGCTCTGGGTGTGAGATATTACTAGTACCAATGCAATTTCTTCAC 352
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCTATAAGAGCAGAAAAAGAAACACTT 360
Db 353 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCTATAAGAGCAGAAAAAGAAACACTT 412
QY 361 CTTTCATGATGAGTTGACTCAATTTACACATTTCCAAAGCTCAGATTGGTCCAC 420
Db 413 CTTTCATGATGAGTTGACTCAATTTACACATTTCCAAAGCTCAGATTGGTCCAC 472
QY 421 AAGTACATTTAGAGCTGAAGATAAGCAATAGTGATACACATCTCTCCTGGAAACAAAG 480
Db 473 AAGTACATTTAGAGCTGAAGATAAGCAATAGTGATACACATCTCTCCTGGAAACAAAG 532
QY 481 ATAGTGTATGTGGGCTTTGCGTGTGTTAAGCTTTACATATAGCTTACTTATCTGAAAA 540
Db 533 ATAGTGTATGTGGGCTTTGCGTGTGTTAAGCTTTACATATAGCTTACTTATCTGAAAA 592
QY 541 ACTCTTCAGGTGTAGAAAGAGGATTGAAAAATTTTATCCAGACATAAAATTTATAAAC 600
Db 652 ACTCTTCAGGTGTAGAAAGAGGATTGAAAAATTTTATCCAGACATAAAATTTATAAAC 652
QY 601 TCTCCGAGACTACTTATGTCTAAAGTTAAGCAGCAGCTACTTACGTATGAAAA 660
Db 712 TCTCCGAGACTACTTATGTCTAAAGTTAAGCAGCAGCTACTTACGTATGAAAA 712
QY 720 TTGGTGTCTATAGTCCAGTACATTTGATAAAGACCAGTTGAAATGAACCTACCTCCAC 720
Db 772 TTGGTGTCTATAGTCCAGTACATTTGATAAAGACCAGTTGAAATGAACCTACCTCCAC 772
QY 780 CAGAAATATPAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780
Db 832 CAGAAATATPAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTATACAT 832
QY 840 ATGCAACATGACTTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGGAATCTCGGAA 840
Db 892 ATGCAACATGACTTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGGAATCTCGGAA 892
QY 900 ACCATTGTATAAATGAAACCAATACCTGACTGTGAAATGTCMAAACTACCCAGTGTG 900
Db 952 ACCATTGTATAAATGAAACCAATACCTGACTGTGAAATGTCMAAACTACCCAGTGTG 952
QY 960 TCTTCTCCTCAAAACGTTTTTCCAAAAAGGAAATTTACCTTCTCCGCGTACAGCATCTGATG 960
Db 1012 TCTTCTCCTCAAAACGTTTTTCCAAAAAGGAAATTTACCTTCTCCGCGTACAGCATCTGATG 1012
QY 1020 GAAATACACATCTTTTGTGCTGAAGAGATAAAGTTTGATCTGAAATACAGCTTTCC 1020
Db 1072 GAAATACACATCTTTTGTGCTGAAGAGATAAAGTTTGATCTGAAATACAGCTTTCC 1072
QY 1080 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTGTGATTCATTTCCATATCTATATCGGTG 1080
Db 1132 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTGTGATTCATTTCCATATCTATATCGGTG 1132
QY 1081 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTATCCATGATTTATGAAATTA 1140
Db 1192 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTATCCATGATTTATGAAATTA 1192
QY 1200 TTTTGTGGGAAAAACATTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200
Db 1252 TTTTGTGGGAAAAACATTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252
QY 1260 CAGTCTCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1260
Db 1312 CAGTCTCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1312
QY 1261 ATGAAAAAGCTGAATAAAGCAGTGTGTTTATAGTCACGCTGTATGTGAGAAAAAACCAG 1320
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## RESULT 2

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US-11-000-688-72
; Sequence 72, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGUETTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(269)
; OTHER INFORMATION: 5' terminal sequence from clone
; OTHER INFORMATION: image:121365, interferon (alpha, beta and omega)
; OTHER INFORMATION: receptor 1 (IFNARI) gene.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (254)..(254)
; OTHER INFORMATION: n is a, c, g, or t
US-11-000-688-72
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Query Match 15.3%; Score 205.6; DB 8; Length 269;

Best Local Similarity 95.5%; Pred. No. 3.3e-46;

Matches 233; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 611 GACTACTTATTGTCTAAAAAGTTAAAGCAGCAGCTACTTACGTATGAAAAATTCGTGTCTA 670

Db 1 GACTACTTATTGTCTAAAAAGTTAAAGCAGCAGCTACTTACGTATGAAAAATTCGTGTCTA 60

QY 671 TAGTCCAGTACATTTGTATTAAGACCAACAGTTCGAAATGAACCTCCACCAAAATAT 730

Db 61 TAGTCCAGTACATTTGTATTAAGACCAACAGTTCGAAATGAACCTCCACCAAAATAT 120

QY 731 AGAAGTCAGTCTCCAAAAATCAGAACTATCTTCTTAAATGGGATTATACATATCAAAACAT 790

Db 121 AGAAGTCAGTCTCCAAAAATCAGAACTATCTTCTTAAATGGGATTATACATATCAAAACAT 180

QY 791 GACCTTTT-CAAGTTCAGT-GGCTCCACGCTTTTAAAAAGGAATCCTGGAAACCAATTTG 848

Db 181 GACCTTTTCAAGTTCAGTGGGCTCCACGCTTTTAAAAAGGAATCCTGGAAACCAATTT 240

QY 849 TATA 852

Db 241 GTTA 244

## RESULT 3

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US-11-128-061-2285
; Sequence 2285, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
```

```
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2285
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-2285

Query Match      15.2%; Score 204.2; DB 8; Length 472;
Best Local Similarity 64.9%; Pred. No. 1.1e-45;
Matches 302; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

Qy 460 ACATCTCTCTCGGAACAAAAGATAGTGTATGTGGGCTTTGGATGGTTTAAAGCTTTTACAT 519
Db 7 ACATCTCTCTATCCGGACAAAGTGGGAAGATGTGTCAGGATATTTCTTCGCTTCGAGT 66

Qy 520 ATAGCTTACTTATCTGGAAAAAAGTCTTTCAGGTGTAGAGAAAGGATTTGAAATATTTATT 579
Db 67 ACAGGGTAGTAATCTGGCAGAAAGTCTTCCAAATGAGACACAGAGTATTACAACCACTTATT 126

Qy 580 CCAGACATAAAATTTATAAAGTCTTCCAGAGACTTACTTATGTCTAAAGTTAAAGCAG 639
Db 127 ATACAGAAAAGATTTCAAAAAGTGTGCGCAGAGACTTACTTGTGTAAAGTTAAAGCAA 186

Qy 640 CACTTACTTACGTATGGAATAAGTGTCTATAGTCCAGTACATTTGTATAAAGACCAAG 699
Db 187 TACATTGCTCCCTCGGGAACACAGCAATTAATGTGAGTGCATGTATATAACCACTATT 246

Qy 700 TTGAAAATGAAGTACTCTCCAGCAAGATATAGAAAGTCAAGTGTCCAAAATCAGAACTATG 759
Db 247 AGGCATCAAGATGCCAGTCCGGAACATATATAAGTGGATGCCCGTGGTGGAGCTATG 306

Qy 760 TTCTTAAATGGGATTTACATATGCAAAACATGACCTTTCAAGTTTCAGTGGCTCCAGCCT 819
Db 307 TTCTGAAATGGGACTGTGCGTCTACAGACGTGAGCTTTCAGAACGCGAGTGGCTCCCTGGCT 366

Qy 820 TTTTAAAAAGGATCCCTGGAAACCATTTGTATTAATGGAACCAATACCTGACTGTGAAA 879
Db 367 ATTTTAAAGTATCTCTGGAAGCTCTTCAATGAATGGAACCAATACCTACCTGTGCGAG 426

Qy 880 ATGTCAAAATACCCAGTGTGTCTTTCTCTCAAAACGTTTTTCCAAA 924
Db 427 ATGTCAAAATACCCAGTGTGTCTTTTCTTAAACACCAATCCACA 471

RESULT 5
US-11-000-688-71/c
; Sequence 71, Application US/11/000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 71
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer

; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2285
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-2285

Query Match      15.2%; Score 204.2; DB 8; Length 472;
Best Local Similarity 64.9%; Pred. No. 1.1e-45;
Matches 302; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

Qy 460 ACATCTCTCTCGGAACAAAAGATAGTGTATGTGGGCTTTGGATGGTTTAAAGCTTTTACAT 519
Db 7 ACATCTCTCTATCCGGACAAAGTGGGAAGATGTGTCAGGATATTTCTTCGCTTCGAGT 66

Qy 520 ATAGCTTACTTATCTGGAAAAAAGTCTTTCAGGTGTAGAGAAAGGATTTGAAATATTTATT 579
Db 67 ACAGGGTAGTAATCTGGCAGAAAGTCTTCCAAATGAGACACAGAGTATTACAACCACTTATT 126

Qy 580 CCAGACATAAAATTTATAAAGTCTTCCAGAGACTTACTTATGTCTAAAGTTAAAGCAG 639
Db 127 ATACAGAAAAGTTCAAAAGTGTGCGCAGAGACTTACTTGTGTAAAGTTAAAGCAA 186

Qy 640 CACTTACTTACGTATGGAATAAGTGTCTATAGTCCAGTACATTTGTATAAAGACCAAG 699
Db 187 TACATTGCTCCCTCGGGAACACAGCAATTAATGTGAGTGCATGTATATAACCACTATT 246

Qy 700 TTGAAAATGAAGTACTCTCCAGCAAGATATAGAAAGTCAAGTGTCCAAAATCAGAACTATG 759
Db 247 AGGCATCAAGATGCCAGTCCGGAACATATATAAGTGGATGCCCGTGGTGGAGCTATG 306

Qy 760 TTCTTAAATGGGATTTACATATGCAAAACATGACCTTTCAAGTTTCAGTGGCTCCAGCCT 819
Db 307 TTCTGAAATGGGACTGTGCGTCTACAGACGTGAGCTTTCAGAACGCGAGTGGCTCCCTGGCT 366

Qy 820 TTTTAAAAAGGATCCCTGGAAACCATTTGTATTAATGGAACCAATACCTGACTGTGAAA 879
Db 367 ATTTTAAAGTATCTCTGGAAGCTCTTCAATGAATGGAACCAATACCTACCTGTGCGAG 426

Qy 880 ATGTCAAAATACCCAGTGTGTCTTTCTCTCAAAACGTTTTTCCAAA 924
Db 427 ATGTCAAAATACCCAGTGTGTCTTTTCTTAAACACCAATCCACA 471

RESULT 4
US-11-128-061-5927
; Sequence 5927, Application US/11/128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(387)
; OTHER INFORMATION: 3' terminal sequence from clone
; OTHER INFORMATION: image:121265, interferon (alpha, beta and omega)
; OTHER INFORMATION: receptor 1 (IFNAR1) gene.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (291)..(292)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (309)..(309)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (312)..(312)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (323)..(323)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (331)..(331)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (346)..(346)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (364)..(364)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (381)..(381)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-000-688-71
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Query Match 4.0%; Score 53.4; DB 8; Length 387;
Best Local Similarity 75.0%; Pred. No. 9e-05;
Matches 90; Conservative 0; Mismatches 26; Indels 4; Gaps 2;

QY 1078 GTGCTCAAAACAGCTCGGAAACACGCC---TGATGATCCAGGATTAT-CCACTGATTAT 1133
Db 325 GCNCCAAACAGCNCNGGAAACACGCCCTGTGNNCCCCAGGATTATCCCACTGATTAT 266

QY 1134 GAAATATTTTTTGGGAAACACTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAAACT 1193
Db 265 GAAATATTTTTTGGGAAACACTTCAAATGCTGAGGTAAGAAAGACTGTATAGTATAATT 206
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RESULT 6
US-10-750-185-21506/c
; Sequence 21506, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
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; SEQ ID NO 21506
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Bovine MMBT10464
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(47)
; OTHER INFORMATION: n is any nucleotide
; US-10-750-185-21506
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Query Match 3.0%; Score 40.8; DB 7; Length 598;
Best Local Similarity 48.3%; Pred. No. 0.3;
Matches 111; Conservative 1; Mismatches 118; Indels 0; Gaps 0;

QY 436 CTGAAGATAAGGCAATAGTGATACACATCTCTCTCGAACAAGAGATAGTGTATGTGGG 495
Db 505 CTAAAGAATAAATATTAGTATACAAAGCTAAATATTTCTGTACAAATATTTATCCCT 446
QY 496 CTTTGATGGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAAGAACTCTTCAGGTGTAG 555
Db 445 TCTAGGAGATATTCAGAGAGTTATTTTCTAGTTTCTTAGAAGAAATTCATTGGTCTAG 386
QY 556 AGAAAGGATTGAAATATTTATTCAGACATAAAATTTATAAATCTCTCACAGAGACTA 615
Db 385 TATAATTTTACCACATGCCCTATTTAAAAACAATAAATTAGAAATTTAAAAACAGTATT 326
QY 616 CTTATTGCTCTAAAGTTAAAGCAGCACTACTTACGTCATCGGAAAAATGGT 665
Db 325 ATATTGTATACCTCTGTAAGCTGTACTCTTTTCTCTTAATGTGGT 276
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RESULT 7
US-10-750-623-21506/c
; Sequence 21506, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 21506
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Bovine MMBT10464
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(47)
; OTHER INFORMATION: n is any nucleotide
; US-10-750-623-21506
```

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Query Match 3.0%; Score 40.8; DB 7; Length 598;
Best Local Similarity 48.3%; Pred. No. 0.3;
Matches 111; Conservative 1; Mismatches 118; Indels 0; Gaps 0;

QY 436 CTGAAGATAAGGCAATAGTGATACACATCTCTCTCGAACAAGAGATAGTGTATGTGGG 495
Db 505 CTAAAGAATAAATATTAGTATACAAAGCTAAATATTTCTGTACAAATATTTATCCCT 446
QY 496 CTTTGATGGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAAGAACTCTTCAGGTGTAG 555
Db 445 TCTAGGAGATATTCAGAGAGTTATTTTCTCTAGTTTCTTAGAAGAAATTCATTGGTCTAG 386
```





Db 569 TAAATTTGTTCAAGAGGTTAAATAAAAGACCTTAGGAATAATTTGCCCCCTCTGTTTATAT 628  
Qy 518 ATATAGCTTACTTATCTGGAATAAACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTA 577  
Db 629 ATATACAAATATAAATTTTAAAGTTTCTATTTTGTGTAAATTTACATTTTAAATATACATAAA 688  
Qy 578 TTCCAGACATATAAATTTTATAAATCTCTCACCAGAGACTACTTATTGTCTTAAAGTTAAAGC 637  
Db 689 TCCCTAAATAATATAATAATAATAATGACATTAATAATCATGCAAGTTTAAATAGTCAATGT 748  
Qy 638 AGCACTACTTACGTCATGGAAAAAT 662  
Db 749 TGATACACTTCCATTTTAAATATAAT 773

RESULT 11  
US-10-750-623-51728  
; Sequence 51728, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 51728  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Bovine 19866880461197  
US-10-750-623-51728

Query Match 2.9%; Score 39.4; DB 7; Length 1542;  
Best Local Similarity 43.9%; Pred. No. 1.2;  
Matches 169; Conservative 0; Mismatches 216; Indels 0; Gaps 0;  
Qy 278 TACCAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAATTAATAATTCGCTAT 337  
Db 389 TATAAATCTACTCTGCTTTATCAATATAAACCATTGAGGAATTAATCTTGGAAAA 448  
Qy 338 AAGAGCAAAAGAAACAACTCTTTCATCGTATGAGGTTGATCTCAATTTACACCATTTTCG 397  
Db 449 AATAGTACAAATGTTTGTATTTTATTTATTAAGATTAATTCACATTAATCTGCAA 508  
Qy 398 CAAAGCTCAGATTGGTCTCCAGAGTACATTTTAGAGCTGAAGATAAGCAATAGTAT 457  
Db 509 GTATTAATTTTACTTTTAATAGGAAACTAATATGATGTTCTTCTTCAAGGGGTT 568  
Qy 458 ACACATCTCTCTGGAACAAAGATAGTGTATGTGGCTTTGGATGGTTTAAAGCTTAC 517  
Db 569 TAATTTGTTCAAGAGGTTAATAAAGACCTTAGGAATAATTTGCCCTCTCTGTTTATAT 628  
Qy 518 ATATAGCTTACTTATCTGGAATAAACTCTTCAGGTGTAGAGAAAGGATGCAAAATATTTA 577  
Db 629 ATATACAAATATAAATTTTAAAGTTTCTATTTTGTGTAAATTAATTTTAAATATACATAA 688  
Qy 578 TTCCAGACATAAATTTTATAAATCTCTCACCAGAGACTACTTATTGTCTTAAAGTTAAAGC 637  
Db 689 TCCCTAAATAATATAATAATAATGACATTAATAATCATGCAAGTTTAAATAGTCAATGT 748  
Qy 638 AGCACTACTTACGTCATGGAAAAAT 662  
Db 749 TGATACACTTCCATTTTAAATATAAT 773

RESULT 12  
US-10-636-716-47  
; Sequence 47, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24CI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1659 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1659  
; OTHER INFORMATION:  
US-10-636-716-47

Query Match 2.9%; Score 39.4; DB 7; Length 1659;  
Best Local Similarity 49.8%; Pred. No. 1.3;  
Matches 128; Conservative 0; Mismatches 126; Indels 3; Gaps 1;  
Qy 198 AATGTGACCTTTTTCATTCGATTATCAAAAACTGGATCGAATAATGGATAAAATTTGCT 257  
Db 196 AAGGTTACTTACTGTGCGAGTATTTTATTTATGGCAGAGAAGTGGCTGAATAAGTCA 255  
Qy 258 GGGTGTGAGATATTACTAGTACCAGAACTTTTCTTCACTCAAGCTGAATGTTAT 317  
Db 256 GAGTGTGAGAAATATCAATCGAACCTATTGTGATCTTCTGCTGAGACTTCTGATATGAG 315  
Qy 318 GAAGAATTAATTTGGTATTAAGAGCAAAAAAACAACCTTCTTC----ATGGTATGAG 374

Db 316 CATCAGTATTATGCCAAGTTTAAGGCCATTGGGGACGAAAGTGTTCACAGTGGGCTGAG 375  
Qy 375 GTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGGTCTCCAGAAAGTACATTTAGAA 434  
Db 376 AGTGGCGGTTTTATCTCTTTCTAGAGACGAGATTGGCCGCGGAGGTGGCGCTGACT 435  
Qy 435 GCTGAAGATAAGGCAAT 451  
Db 436 ACGGATGGAAGTCCAT 452

## RESULT 13

US-10-750-185-25730/c

; Sequence 25730, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25730

; LENGTH: 4419

; TYPE: DNA

; ORGANISM: Bovine 19866881150821

US-10-750-185-25730

Query Match 2.9%; Score 39.4; DB 7; Length 4419;  
Best Local Similarity 45.2%; Pred. No. 2.2;  
Matches 145; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 572 TATTATTCCAGACATAAAATTTATAAACTCTCCAGAGACTACTTATTGCTTAAAGT 631  
Db 733 TAATTAGAAAATACTAAATATACAATCTAGTCTTTTCATTCTTTCTCGATAAATAG 674  
Qy 632 TAAAGCAGCACTACTTACGTCATGGAATAATGGTGCTATAGTCCAGTACATTTGTATATA 691  
Db 673 TAGAAGGACATTTTAAAGTAAGATGAATTTGATGTTCTTAAGCATATTAATTTAGAAAA 614  
Qy 692 GACCACAGTTGAAAATGAATACCTCCACCAGAAAATATAGAACTAGTGTCCAAAATCA 751  
Db 613 GACCATTACATAAGACAGAAATTTATTTTCTTAAACATTTTAAATCACTGGATAATATCC 554  
Qy 752 GAACATGTTCTTAAATGGGATTATACATATGCAAAACATGACCTTCAAGTTTCAGTGGCT 811  
Db 553 TATTGTTTCATATTATGTTTATGGGAAAATATGATCTTATTTTCTAGTTTGTATGCT 494  
Qy 812 CCAGCGCTTTTAAAAAGGAATCCTCGAAACCAATTTGTATATAATGGAACAAATACCTGA 871  
Db 493 AGAGTCCTTTTTTAAATCCAAATAGCATATATTTAATATATGCAATTTTGAAAAGTTAC 434  
Qy 872 CTGTGAAAATGTCAAAACTAC 892  
Db 433 CTTTTCAAAATCATAACTAC 413

## RESULT 14

US-10-750-623-25730/c

; Sequence 25730, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25730  
; LENGTH: 4419  
; TYPE: DNA  
; ORGANISM: Bovine 19866881150821  
US-10-750-623-25730

Query Match 2.9%; Score 39.4; DB 7; Length 4419;  
Best Local Similarity 45.2%; Pred. No. 2.2;  
Matches 145; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 572 TATTATTCCAGACATAAAATTTATAAACTCTCCAGAGACTACTTATTGCTTAAAGT 631  
Db 733 TAATTAGAAAATACTAAATATACAATCTAGTCTTTTCATTCTTTCTCGATAAATAG 674  
Qy 632 TAAAGCAGCACTACTTACGTCATGGAATAATGGTGCTTATAGTCCAGTACATTTGTATATA 691  
Db 673 TAGAAGGACATTTTAAAGTAAGATGAATTTGATGTTCTTAAGCATATTAATTTAGAAAA 614  
Qy 692 GACCACAGTTGAAAATGAATACCTCCACCAGAAAATATAGAACTAGTGTCCAAAATCA 751  
Db 613 GACCATTACATAAGACAGAAATTTATTTTCTTAAACATTTTAAATCACTGGATAATATCC 554  
Qy 752 GAACATGTTCTTAAATGGGATTATACATATGCAAAACATGACCTTCAAGTTTCAGTGGCT 811  
Db 553 TATTGTTTCATATTATGTTTATGGGAAAATATGATCTTATTTTCTAGTTTGTATGCT 494  
Qy 812 CCAGCGCTTTTAAAAAGGAATCCTCGAAACCAATTTGTATATAATGGAACAAATACCTGA 871  
Db 493 AGAGTCCTTTTTTAAATCCAAATAGCATATATTTAATATATGCAATTTTGAAAAGTTAC 434  
Qy 872 CTGTGAAAATGTCAAAACTAC 892  
Db 433 CTTTTCAAAATCATAACTAC 413

## RESULT 15

US-11-112-908-20

; Sequence 20, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 20

; LENGTH: 191331

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-20

Query Match	2.9%	Score 38.8;	DB 8;	Length 191331;
Best Local Similarity	51.1%	Pred. No. 26;		
Matches 91;	Conservative 0;	Mismatches 87;	Indels 0;	Gaps 0;

  

Qy	564	ATTGAAATATTATTCAGACATATAAAATTTATAAACTCTCACGAGAGACTACTTATTGT	623
Db	110325	AATGAAAAATTTACTTTCTGACCTGACATTCAACATCTTTCACTTGAACAAAAACATCTG	110384

  

Qy	624	CTAAAGTTAAAGCAGCACTACTTACGTCATGGAAATTTGGTCTCTATAGTCAGTACAT	683
Db	110385	ATTTAGTTCTAGATCTGCCACTTACATTACTGAGAAAGTCATTGATGGCTCAGAACCA	110444

  

Qy	684	TGTATAAGACCAACAGTTGAAATGAACTACCTCCACGAGAAATATAGAAAGTCAGTG	741
Db	110445	TCTGTGAAGTGGGACATCATATATACCACCTTGTTAAGTCATTGTGAAAAATATGAG	110502

Search completed: January 18, 2006, 02:12:44  
Job time : 315 secs



[illegible]

Db 1 CTGCGGGATCTGCGGGGCTCCAGATGATGCTGCTCTCTGCGGGCGGACGCCCTAG 60  
Qy 61 TGCTCGTGGCGGCGCCATGGGTGTTGTCGCGAGCGCGAGGTGGAAAAATCTAAAT 120  
Db 61 TGCTCGTGGCGGCGCCATGGGTGTTGTCGCGAGCGCGAGGTGGAAAAATCTAAAT 120  
Qy 121 CTCCTCAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA 180  
Db 121 CTCCTCAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA 180  
Qy 181 GCGATGAGTCTGTCGGGAATGAGCTTTTCATTCGATATCAAAAACTGGGATGGATA 240  
Db 181 GCGATGAGTCTGTCGGGAATGAGCTTTTCATTCGATATCAAAAACTGGGATGGATA 240  
Qy 241 ATTGGATAAAATTTCTGCGGTGTCAGAAATTTACTAGTACAAATGCAACTTTTCTTCC 300  
Db 241 ATTGGATAAAATTTCTGCGGTGTCAGAAATTTACTAGTACCAATGCAACTTTTCTTCC 300  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTTAAATTGCGGTATAGAGCAGAAAAAGAAACACTT 360  
Db 301 TCAAGCTGAATGTTTATGAAGAAATTTAAATTGCGGTATAGAGCAGAAAAAGAAACACTT 360  
Qy 361 CTTCATGATGAGGTGACCTCATTTACCACTTTGCGAAAGCTCAGATTGGTCTCCAG 420  
Db 361 CTTCATGATGAGGTGACCTCATTTACCACTTTGCGAAAGCTCAGATTGGTCTCCAG 420  
Qy 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACATCTCTCTGGAACAAAAG 480  
Db 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACATCTCTCTGGAACAAAAG 480  
Qy 481 ATAGTGTATGCGGCTTTGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA 540  
Db 481 ATAGTGTATGCGGCTTTGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA 540  
Qy 541 ACTCTTCAGGTGATGAAGAAAGGTTGAATATTTATTCAGACATATAATTTATAAC 600  
Db 541 ACTCTTCAGGTGATGAAGAAAGGTTGAATATTTATTCAGACATATAATTTATAAC 600  
Qy 601 TCTCAGCAGACTACTTATTTGCTTAAAGTTAAAGCAGCAGCTACTTACGTCACTGAAAA 660  
Db 601 TCTCAGCAGACTACTTATTTGCTTAAAGTTAAAGCAGCAGCTACTTACGTCACTGAAAA 660  
Qy 720 TTGTTGCTATAGTCCAGTACATTTGATTAAGACACAGTTGAAATGAATCACTCCAC 720  
Db 661 TTGTTGCTATAGTCCAGTACATTTGATTAAGACACAGTTGAAATGAATCACTCCAC 720  
Qy 721 CAGAAATATAGAGTCAAGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
Db 721 CAGAAATATAGAGTCAAGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
Qy 781 ATGCAACATGACCTTTCAAGTTCAAGTCCAGCTCCAGCCCTTTTAAAGAGGAATCTCGAA 840  
Db 781 ATGCAACATGACCTTTCAAGTTCAAGTCCAGCTCCAGCCCTTTTAAAGAGGAATCTCGAA 840  
Qy 841 ACCATTTCTATAAATGAAAAAATACTGACTGTGAAAAATGTCAAAACTACCCAGTGTG 900  
Db 841 ACCATTTCTATAAATGAAAAAATACTGACTGTGAAAAATGTCAAAACTACCCAGTGTG 900  
Qy 901 TCTTCTCTCAAAACGTTTTTCAAAAGGAATTTACCTTCTCGCGGTACAAGCATCTGATG 960  
Db 901 TCTTCTCTCAAAACGTTTTTCAAAAGGAATTTACCTTCTCGCGGTACAAGCATCTGATG 960  
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAGTTTGATCTCAAACTCAAGCTTTCC 1020  
Db 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAGTTTGATCTCAAACTCAAGCTTTCC 1020  
Qy 1021 TACTTCTCTCAAGTCTTTAAACATTAGATCCCTTAGTGATTTCAATTCATATCTATATCGGTG 1080  
Db 1021 TACTTCTCTCAAGTCTTTAAACATTAGATCCCTTAGTGATTTCAATTCATATCTATATCGGTG 1080  
Qy 1081 CTCCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTAATCCACTGATTTATGAAATTA 1140  
Db 1081 CTCCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTAATCCACTGATTTATGAAATTA 1140

Qy 1141 TTTTGTGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1141 TTTTGTGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Qy 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTTGAAAGCCAGAGCAGACACCATGG 1260  
Db 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTTGAAAGCCAGAGCAGACACCATGG 1260  
Qy 1261 ATGAAAAAGCTGAATAAAAGCAGTGTGTTTATGTCGCTGTATGTCGAGAAAAACAAACCCAG 1320  
Db 1261 ATGAAAAAGCTGAATAAAAGCAGTGTGTTTATGTCGCTGTATGTCGAGAAAAACAAACCCAG 1320  
Qy 1321 GAAATACCTCTTAATGAGGTACC 1343  
Db 1321 GAAATACCTCTTAATGAGGTACC 1343

## RESULT 3

US-09-240-675-3  
; Sequence 3, Application US/09240675  
; Patent No. US20020055492A1  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,675  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1755 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 27..1697  
US-09-240-675-3



Query Match					
Best Local Similarity 99.3%; Score 1334; DB 3; Length 1755;					
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	CTGCAGGGATCTGCGGGCTCCACAGATGATGGTCCTCGGCGCGACGCCCTTAG	60		
Dd	1	CTGCAGGGATCTGCGGGCTCCACAGATGATGGTCCTCGGCGCGACGCCCTTAG	60		
Qy	61	TGCTCGTCCGCGTGGGCCCATGGGTGTGTCCGACGCGCAGGTGGAAAAAATCTAAAT	120		
Dd	61	TGCTCGTCCGCGTGGGCCCATGGGTGTGTCCGACGCGCAGGTGGAAAAAATCTAAAT	120		
Qy	121	CTCTCAAAAAGTAGAGTGACATCATAGATGACAATTATCCTGAGGTGGAACAGGA	180		
Dd	121	CTCTCAAAAAGTAGAGTGACATCATAGATGACAATTATCCTGAGGTGGAACAGGA	180		
Qy	181	GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTTCGATTATCAAAAAACTGGGATGATA	240		
Dd	181	GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTTCGATTATCAAAAAACTGGGATGATA	240		
Qy	241	ATTGGATAAAATTCGTCTGGGTGTCAGAATAATTACTAGTACCAAATGCACTTTTCTTCAC	300		
Dd	241	ATTGGATAAAATTCGTCTGGGTGTCAGAATAATTACTAGTACCAAATGCACTTTTCTTCAC	300		
Qy	301	TCAAGCTGAATGTTTTATGAAGAAATTAATTCGTATAAGACGAGAAAAAGAACACTT	360		
Dd	301	TCAAGCTGAATGTTTTATGAAGAAATTAATTCGTATAAGACGAGAAAAAGAACACTT	360		
Qy	361	CTTTCATGGTATGAGGTTGACTCATTTACACATTTCCGAAAGCTCAGATTGGTCTCCAG	420		
Dd	361	CTTTCATGGTATGAGGTTGACTCATTTACACATTTCCGAAAGCTCAGATTGGTCTCCAG	420		
Qy	421	AAGTACATTTAGAAAGCTGAAGATAAGCAATPAGTGATACACATCTCTCTGGAAACAAAG	480		
Dd	421	AAGTACATTTAGAAAGCTGAAGATAAGCAATPAGTGATACACATCTCTCTGGAAACAAAG	480		
Qy	481	ATAGTGTATTGTGGGCTTTGGATGGTTTAAAGCTTTACATAGCTTACTTATCTGGAAAA	540		
Dd	481	ATAGTGTATTGTGGGCTTTGGATGGTTTAAAGCTTTACATAGCTTACTTATCTGGAAAA	540		
Qy	541	ACTCTTCAGGTGTAGAAAGAAAGATGAAATAATTTATTCAGACATAAAATTTATAAAC	600		
Dd	541	ACTCTTCAGGTGTAGAAAGAAAGATGAAATAATTTATTCAGACATAAAATTTATAAAC	600		
Qy	601	TCTCACAGAGACTTACTTATTTGCTCTAAAGTTAAAGCAGCACTTACTCGTCATGGAAA	660		
Dd	601	TCTCACAGAGACTTACTTATTTGCTCTAAAGTTAAAGCAGCACTTACTCGTCATGGAAA	660		
Qy	661	TTGGTGTCTATAGTCCAGTACATTTGATTAAGACACAGTTTGAATATGAATCTCTCCAC	720		
Dd	661	TTGGTGTCTATAGTCCAGTACATTTGATTAAGACACAGTTTGAATATGAATCTCTCCAC	720		
Qy	721	CAGAAAAATAGAAAGTCAAGTGTCAAATCAGAACTATGTTCTTTAAATGGGATPATACAT	780		
Dd	721	CAGAAAAATAGAAAGTCAAGTGTCAAATCAGAACTATGTTCTTTAAATGGGATPATACAT	780		
Qy	781	ATGCABAACATGACCTTTTCAAGTTCAGTGGCTCCAAGCTTTTAAAGGAATCCTGGAA	840		
Dd	781	ATGCABAACATGACCTTTTCAAGTTCAGTGGCTCCAAGCTTTTAAAGGAATCCTGGAA	840		
Qy	841	ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAAATGTCAAACCTACCCAGGTG	900		
Dd	841	ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAAATGTCAAACCTACCCAGGTG	900		
Qy	901	TCCTTCTCAAAACGTTTTTCAAAAAGGAATTTTACCTTCTCCGCGTCAAGCATCTGATG	960		
Dd	901	TCCTTCTCAAAACGTTTTTCAAAAAGGAATTTTACCTTCTCCGCGTCAAGCATCTGATG	960		
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Qy	1021	TACTTCTCCAGTCTTTTAAACATTAGATCCCCTTAGTGTATTCATTCATATCTATCCGGT	1080		

RESULT 4  
 US-10-824-981-3  
 ; Sequence 3, Application US/10824981  
 ; Publication No. US20040191840A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benoit, Patrick  
 ; APPLICANT: Maguire, Deborah  
 ; APPLICANT: Plavec, Ivan  
 ; APPLICANT: Tovy, Michael  
 ; APPLICANT: Meyer, Francois  
 ; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With  
 ; FILE REFERENCE: A-72230-2  
 ; CURRENT APPLICATION NUMBER: US/10/824,981  
 ; CURRENT FILING DATE: 2004-04-14  
 ; PRIOR APPLICATION NUMBER: US 09/240,675  
 ; PRIOR FILING DATE: 1999-02-02  
 ; PRIOR APPLICATION NUMBER: US 08/307,588  
 ; PRIOR FILING DATE: 1994-12-05  
 ; PRIOR APPLICATION NUMBER: PCT/EP93/00770  
 ; PRIOR FILING DATE: 1993-03-30  
 ; PRIOR APPLICATION NUMBER: EP 92400902.0  
 ; PRIOR FILING DATE: 1992-03-31  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 3  
 ; LENGTH: 1755  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (27)..(1697)  
 US-10-824-981-3

	Query Match	99.2%	Score 1332.4	DB 8	Length 1755	
	Best Local Similarity	99.9%	Pred. No. 0			
	Matches 1333	Conservative 0	Mismatches 1	Indels 0	Gaps 0	
Qy	1	CTGCAGGGATCTCGGGCGGTCTCCAGATGATGTGCTCTCTCTGGGCGCGACGACCCCTAG	60			
Db	1	CTGCAGGGATCTCGGGCGGTCTCCAGATGATGTGCTCTCTCTGGGCGCGACGACCCCTAG	60			
Qy	61	TGCTCGTCTGCGGTGGGGCCATGGTGTGTCTCGCAGCGCGAGGTGGAAAAAATCTCAAAT	120			
Db	61	TGCTCGTCTGCGGTGGGGCCATGGTGTGTCTCGCAGCGCGAGGTGGAAAAAATCTCAAAT	120			
Qy	121	CTCTCAAAAAGTAGAGGTTCGACATCATAGATGACAACTTTATCTCTGAGGTGGAAACGAGGA	180			
Db	121	CTCTCAAAAAGTAGAGGTTCGACATCATAGATGACAACTTTATCTCTGAGGTGGAAACGAGGA	180			

Qy 181 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTTCGATTATCAAAAAAAGTGGATGGATA 240  
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Qy 241 ATTGGATAAATGCTGCGGTGTCAGATATTAAGTACCAATGCAATCTTCTTCAC 300  
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Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATATGCGGTATAAGAGCAGAAAAAGAAACACTT 360  
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Qy 361 CTTCAATGATGAGTTGACTCAATTTACCAATTTGCAAAAGCTCAGATTGGTCTCCAG 420  
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Qy 481 ATAGTGTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540  
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Db |||||||  
Qy 841 ACCATTTGATAAATGGAACAATACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
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Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAGTTTGATACCTGCTGCTGCTGCTGCTGCTG 1020  
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Qy 1081 CTCCAAAAACAGTCTGGAACAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
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Qy 1261 ATGAAAAGCTGAATAAAGCAGCTGTTTATGAGCTGTATGTGAGAAAAAACAACCCAG 1320  
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Qy 1321 GAAATACCTCTAAA 1334  
Db |||||||  
RESULT 5  
US-10-641-643-1118  
; Sequence 1118, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1118:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2755 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g184645  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1118 :  
US-10-641-643-1118  
Query Match 99.1%; Score 1330.8; DB 7; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Qy 53 CTGCTGCGCTGCGGGCCCATGGGTGTTGTCGCGAGCGCAGGTGGAATAATCTAAAT 120  
Db |||||||  
Qy 61 TGCTGCTGCGCTGCGGGCCCATGGGTGTTGTCGCGAGCGCAGGTGGAATAATCTAAAT 120  
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Qy 121 CTCCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTTATCTGAGGTGGAAACAGGA 180  
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Qy 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAAGTGGATGGATA 240  
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Db 653 TCTCACCAGAGACTACTTATGTCTAAAGTTAAAGTAAAGCAGCACTACTTACGTCATGGAATA 712  
Qy 661 TTGTGTCTATAGTCCAGTACATTTATTAAGACACAGTTGAAATGAAATGAACTACCTCCAC 720  
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Qy 781 ATGCAACATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGAAATCTCGGAA 840  
Db 833 ATGCAACATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGAAATCTCGGAA 892  
Qy 841 ACCATTTGTATAAATGAAACAAATACCTGACTGTGAAATGTCAAACTACCCAGGTG 900  
Db 893 ACCATTTGTATAAATGAAACAAATACCTGACTGTGAAATGTCAAACTACCCAGGTG 952  
Qy 901 TCTTTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGCTACAGCATCTGATG 960  
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RESULT 6  
US-10-888-313A-81  
; Sequence 81, Application US/10888313A  
; Publication No. US20050100934A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, Kevin  
; APPLICANT: AXEL, Richard  
; APPLICANT: STRAPPS, Walter  
; APPLICANT: BARNEA, Gilad  
; TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction  
; FILE REFERENCE: SENTI 203.2  
; CURRENT APPLICATION NUMBER: US/10/888,313A  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/566,113  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: 60/511,918  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/485,968  
; PRIOR FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 101  
; SEQ ID NO 81  
; LENGTH: 2755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-313A-81  
Query Match 99.1%; Score 1330.8; DB 9; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGCGGGATCTCGCGGGCTCCAGATGATGGTCTCTCTGGGGCGGACGCCCTAG 60  
Db 53 CTGCGGGATCTCGCGGGCTCCAGATGATGGTCTCTCTGGGGCGGACGCCCTAG 112  
Qy 61 TGCTCTCCCGCTGGGCCCATGGTCTGTCGCGCAGCGCAGGTGAAATAATCTAAAT 120  
Db 113 TGCTCTCCCGCTGGGCCCATGGTCTGTCGCGCAGCGCAGGTGAAATAATCTAAAT 172  
Qy 121 CTCCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTGAGGTGGAACAGGA 180  
Db 173 CTCCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTGAGGTGGAACAGGA 232  
Qy 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAAGTGGATGGATA 240  
Db 233 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAAGTGGATGGATA 292  
Qy 241 ATTGGATAAAATTCCTGGGGTGTGAGATATTACTAGTACCAATGCAACTTTTCTTCAC 300  
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Db 353 TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGAGCAGAAAAAGAAACACTT 412  
Qy 361 CTTTCATGGTATGAGTTGACTCAATTTACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
Db 413 CTTTCATGGTATGAGTTGACTCAATTTACCAATTCGCAAGCTCAGATTGGTCTCCAG 472  
Qy 421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480  
Db 473 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 532  
Qy 481 ATAGTGTATGTGGCTTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540



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Qy 901 TCTTTCCTCAAAACGTTTTCCAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960
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Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTAGTAATACAAGCTTTCC 1020
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RESULT 8

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US-09-822-830A-38/c
; Sequence 38, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechoel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Reenick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 2278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-38
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Query Match 98.7%; Score 1326; DB 3; Length 2278;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1329; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 61 TGCTCGTCGCGGTGGGCGGATGGTGTGTCGCGCGGCGAGTGGGAAAAAATCTAAAT 120
Db 2153 TGCTCGTCGCGGTGGGCGGATGGTGTGTCGCGCGGCGAGTGGGAAAAAATCTAAAT 2094
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Db 1133 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1074
Qy 1141 TTTTTCGGGAAAACACCTTCAAATGCTGAGAGAAAAAATTTATCGAGAAAAAACTGATGTTA 1200
Db 1073 TTTTTCGGGAAAACACCTTCAAATGCTGAGAGAAAAAATTTATCGAGAAAAAACTGATGTTA 1014
Qy 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTGAAAGCCAGACACACCATGG 1260
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Db	1013	CAGTTCCTAATTTGAAACCACTGACTGCTATATTTGTGTGAAGCCAGAGCACACCATGG	954
Qy	1261	ATGAAAAGCTGAATATAAAGCAGTGTCTTTTATGTCAGCTGTATGTGAGAAAAACAAAACAG	1320
Db	953	ATGAAAAGCTGAATATAAAGCAGTGTCTTTTATGTCAGCTGTATGTGAGAAAAACAAAACAG	894
Qy	1321	GAATACCTCTAAA	1334
Db	893	GAATACCTCTAAA	880
RESULT 9			
US-10-764-833-43			
; Sequence 43, Application US/10764833			
; Publication No. US20040248157A1			
GENERAL INFORMATION:			
; APPLICANT: Ayalon, Michal			
; APPLICANT: Pollock, Sarah			
; APPLICANT: Diber, Alex			
; APPLICANT: Levine, Zurit			
; APPLICANT: Nemzer, Sergey			
; APPLICANT: Dahary, Dvir			
; APPLICANT: Sorek, Rotem			
; APPLICANT: Levanon, Erez			
; APPLICANT: Rotman, Galit			
; APPLICANT: Savitsky, Kineret			
; APPLICANT: Chermesh, Chen			
; APPLICANT: Mintz, Liat			
; APPLICANT: Freilich, Shiri			
; APPLICANT: Beck, Nili			
; APPLICANT: Zhu, Wei-Yong			
; APPLICANT: Wasserman, Alon			
; APPLICANT: Azar, Idit			
; APPLICANT: Bernstein, Jeanne			
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING SOLUBLE POLYPEPTIDES AND METHODS			
; FILE OF INVENTION: SAME			
; FILE REFERENCE: 27256			
; CURRENT APPLICATION NUMBER: US/10/764,833			
; CURRENT FILING DATE: 2004-01-27			
; NUMBER OF SEQ ID NOS: 43			
; SOFTWARE: Patentin version 3.2			
; SEQ ID NO 43			
; LENGTH: 1512			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-764-833-43			
Query Match 97.8%; Score 1313.2; DB 8; Length 1512;			
Best Local Similarity 99.4%; Pred. No. 0;			
Matches 1318; Conservative 0; Mismatches 8; Indels 0; Gaps 0;			
Qy	1	CTGAGGGATCTGGGGCGCTCCAGATGATGGTGTCTCTCTGGCGCGGACCCCTAG	60
Db	127	CTGTGGGATCTGGCGGGCTCCAGATGATGGTGTCTCTCTGGCGCGGACCCCTAG	186
Qy	61	TGCTCGTCGGTGGCGCCATGGGTGTTCGCGAGCGCGAGTGGAAAAATCTAAAAT	120
Db	187	TGCTCGTCGGTGGCGCCATGGGTGTTCGCGAGCGCGAGTGGAAAAATCTAAAAT	246
Qy	121	CTCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA	180
Db	247	CTCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA	306
Qy	181	GGGATGAGTCTGTGGGAATGTGACTTTTTCATTCGATTCATAAAAACTGGGATGGATA	240
Db	307	GGGATGAGTCTGTGGGAATGTGACTTTTTCATTCGATTCATAAAAACTGGGATGGATA	366
Qy	241	ATTGATAAAATGTCTGGGTGTGAGATATTACTAGTACCAAAATGCAACTTTCTTTCAC	300
Db	367	ATTGATAAAATGTCTGGGTGTGAGATATTACTAGTACCAAAATGCAACTTTCTTTCAC	426
Qy	301	TCAAGCTGAATCTTTTATGAAGAAATTTAAATTCGGTATTAAGACGAGAAAAAACAACACTT	360

RESULT 10

Db	427	TCAGCTGAAATGTTATGAAGAAATTTAAATTCGGTATTAAGACGAGAAAAACAACACTT	486
Qy	361	CTTCATGTTATGAGTTGACTCAATTTACACCAATTTGCAAAAGCTCAGATTGGTCTCCAG	420
Db	487	CTTCATGTTATGAGTTGACTCAATTTACACCAATTTGCAAAAGCTCAGATTGGTCTCCAG	546
Qy	421	AAGTACATTTAGAAAGCTGGAAGTAAGGCAATAGTATACATCTCTCTCGGAAACAAAAG	480
Db	547	ARGTACATTTAGAAAGCTGGAAGTAAGGCAATAGTATACATCTCTCTCGGAAACAAAAG	606
Qy	481	ATAGTGTATGTGGGCTTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA	540
Db	607	ATAGTGTATGTGGGCTTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA	666
Qy	541	ACTCTTCAGGTGTAGAAAGGATTTGAAAATATTTTATTCAGACATATAAATTTTATAAAC	600
Db	667	ACTCTTCAGGTGTAGAAAGGATTTGAAAATATTTTATTCAGACATATAAATTTTATAAAC	726
Qy	601	TCTCACCAGAGACTTACTTATTTGTTAAAGCTTAAAGCAGCACTACTTACGTTCATGGAAAA	660
Db	727	TCTCACCAGAGACTTACTTATTTGTTAAAGCTTAAAGCAGCACTACTTACGTTCATGGAAAA	786
Qy	661	TTGGTGTCTATAGTCCAGTACATTTGTATAAAGCACAGATTGAAAAATGAACACTCCTCCAC	720
Db	787	TTGGTGTCTATAGTCCAGTACATTTGTATAAAGCACAGATTGAAAAATGAACACTCCTCCAC	846
Qy	721	CAGAAAAATATAGAAAGTCAGTGTCCAAAATCAGAACTATGTCTTTAAATGGGATTATACAT	780
Db	847	CAGAAAAATATAGAAAGTCAGTGTCCAAAATCAGAACTATGTCTTTAAATGGGATTATACAT	906
Qy	781	ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAAAGGAAATCCTCGAA	840
Db	907	ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAAAGGAAATCCTCGAA	966
Qy	841	ACCAATTTGTATAAATGAAGAAACAAATACCTGACTGTGAAAAATGTCAAACACTACCCAGTGTG	900
Db	967	ACCAATTTGTATAAATGAAGAAACAAATACCTGACTGTGAAAAATGTCAAACACTACCCAGTGTG	1026
Qy	901	TCTTTCTCTCAAAAGCTTTTCCAAAAGGAAATTTACCTTCTCCGGGTCAAGCATCTGATG	960
Db	1027	TCTTTCTCTCAAAAGCTTTTCCAAAAGGAAATTTACCTTCTCCGGGTCAAGCATCTGATG	1086
Qy	961	GAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC	1020
Db	1087	GAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC	1146
Qy	1021	TACTTCTCTCAGTCTTTAAACATTAGATCCCTTAGTGTTCATTCCATATCTATATCGGTG	1080
Db	1147	TACTTCTCTCAGTCTTTAAACATTAGATCCCTTAGTGTTCATTCCATATCTATATCGGTG	1206
Qy	1081	CTCCAAAACAGTCTGGAACACACGCTGTGTATCCAGGATTTCCACTGATTTTATGAAATTA	1140
Db	1207	CTCCAAAACAGTCTGGAACACACGCTGTGTATCCAGGATTTCCACTGATTTTATGAAATTA	1266
Qy	1141	TTTTTTGGGAAAAACATTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA	1200
Db	1267	TTTTTTGGGAAAAACATTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA	1326
Qy	1201	CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACATGG	1260
Db	1327	CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACATGG	1386
Qy	1261	ATGAAAAGCTCAATTAAGAGCAGTGTCTTTTAGTGCAGCTGTATGTGAGAAAAACAAACCCAG	1320
Db	1387	ATGAAAAGCTCAATTAAGAGCAGTGTCTTTTAGTGCAGCTGTATGTGAGAAAAACAAACCCAG	1446
Qy	1321	GAATA	1326
Db	1447	GTGAGA	1452



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US-10-450-763-17285
; Sequence 17285, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; CURRENT FILING DATE: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17285
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (518)..(1837)
; OTHER INFORMATION: 100% homologous to Homo sapiens interferon alpha/beta
; OTHER INFORMATION: receptor, accession number X60459, Smith-Waterman Score=2324.
US-10-450-763-17285

Query Match          97.6%; Score 1310.2; DB 9; Length 2844;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY      1  CTGCGAGGATCTGCGGGCGCTCCAGATGATGGTGGTCTCTCGGGCGGCGAGCACCTAG 60
      |||
Db      140 CTGGTGGATCTGCGGGCGCTCCAGATGATGGTGGTCTCTCGGGCGGCGAGCACCTAG 199
      |||

QY      61  TGTGTGTCGCGCGTGGGCCATGGGTGTTGCCAGCGCCAGGTGGAAAAAATCTAAAT 120
      |||
Db      200 AGCTGTCGCGGTGGGCCATGGGTGTTGCCAGCGCCAGGTGGAAAAAATCTAAAT 259
      |||

QY      121 CTCTCAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 180
      |||
Db      260 CTCTCAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 319
      |||

QY      181 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAAACCTGGCATGGATA 240
      |||
Db      320 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAAACCTGGCATGGATA 379
      |||

QY      241 ATTGGATAAAATGTCTGGGTGTCAGAAATATTACTAGTACCAATGCCAATTTCTTTCAC 300
      |||
Db      380 ATTGGATAAAATGTCTGGGTGTCAGAAATATTACTAGTACCAATGCCAATTTCTTTCAC 439
      |||

QY      301 TCAAGCTGATGTTTATGAGAAATTTAAATGGTATTAAGAGCAGAAAAAGAAACACTT 360
      |||
Db      440 TCAAGCTGATGTTTATGAGAAATTTAAATGGTATTAAGAGCAGAAAAAGAAACACTT 499
      |||

QY      361 CTTTCATGGTATGAGG-ITGACTCATTTACACCACTTCGCAAGCTCAGATTGGTCTCTCCA 419
      |||
Db      500 CTTTCATGGTATGAGGTTGACTCATTTACACCACTTCGCAAGCTCAGATTGGTCTCTCCA 559
      |||

QY      420 GAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCTGGAAACAAA 479
      |||
Db      560 GAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCTGGAAACAAA 619
      |||

QY      480 GATAGTGTATCTGGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAA 539
      |||
Db      620 GATAGTGTATCTGGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAA 679
      |||

QY      540 AACTCTTCAGGTGTAGAGAAAGGATTGAAAAATTTATTTCCAGACATAAAATTTATAA 599
      |||
Db      680 AACTCTTCAGGTGTAGAGAAAGGATTGAAAAATTTATTTCCAGACATAAAATTTATAA 739
      |||

QY      600 CTCTCACCAGAGACTACTTATTGTCTTAAAGTTAAAGCAGCACTACTTACGTCAAGAAA 659
      |||
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## RESULT 11

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US-10-027-632-118153
; Sequence 118153, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
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Db      740 CTCTCACCAGAGACTACTTATTGTCTTAAAGTTAAAGCAGCACTACTTACGTCAATGAAA 799
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QY      660 ATTGGTGTCTATAGTCCAGTACATTTGTATATAGAGACACAGTTGAAATGAACTACCTCCA 719
      |||
Db      800 ATTGGTGTCTATAGTCCAGTACATTTGTATATAGAGACACAGTTGAAATGAACTACCTCCA 859
      |||
QY      720 CCAGAAAAATATAGAAAGTCAAGTGTCCAAAAATCAGAACTATGTTCTTAAATGGGATTTATACA 779
      |||
Db      860 CCAGAAAAATATAGAAAGTCAAGTGTCCAAAAATCAGAACTATGTTCTTAAATGGGATTTATACA 919
      |||
QY      780 TATGCAAAACATGACCTTTTCAAGTTTCAAGTGTCCAGCTCCAGCCCTTTTAAAAAGGAATTCCTGGA 839
      |||
Db      920 TATGCAAAACATGACCTTTTCAAGTTTCAAGTGTCCAGCTCCAGCCCTTTTAAAAAGGAATTCCTGGA 979
      |||
QY      840 AACCATTTCGTATATAGTGAAGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGT 899
      |||
Db      980 AACCATTTCGTATATAGTGAAGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGT 1039
      |||
QY      900 GTCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGAT 959
      |||
Db      1040 GTCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGAT 1099
      |||
QY      960 GGAATAAACAATCTTTTGGTCTGAAGAGATAAAGTTTGAATACTGAAATACAAGCTTTC 1019
      |||
Db      1100 GGAATAAACAATCTTTTGGTCTGAAGAGATAAAGTTTGAATACTGAAATACAAGCTTTC 1159
      |||
QY      1020 CTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGAATTCATTCATATCTATATCGGT 1079
      |||
Db      1160 CTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGAATTCATTCATATCTATATCGGT 1219
      |||
QY      1080 GCTCCAAAAACAGTCTGAAAAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAAT 1139
      |||
Db      1220 GCTCCAAAAACAGTCTGAAAAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAAT 1279
      |||
QY      1140 ATTTTGTGGAAAAACAATCTCAAAATGCTGAGAGAAAAAATTTATCGAGAAAAAACTGATGTT 1199
      |||
Db      1280 ATTTTGTGGAAAAACAATCTCAAAATGCTGAGAGAAAAAATTTATCGAGAAAAAACTGATGTT 1339
      |||
QY      1200 ACAGTTCCTTAATTTGAAACCACTGACTGTATTTGTGTGAAAGCCAGAGCAGACACCATG 1259
      |||
Db      1340 ACAGTTCCTTAATTTGAAACCACTGACTGTATTTGTGTGAAAGCCAGAGCAGACACCATG 1399
      |||
QY      1260 GATGAAAAAGCTCAATAAAACAGTGTGTTTGTAGTGAAGCTGTATGTGAGAAAAACAAAACCA 1319
      |||
Db      1400 GATGAAAAAGCTCAATAAAACAGTGTGTTTGTAGTGAAGCTGTATGTGAGAAAAACAAAACCA 1459
      |||
QY      1320 GGAATACCTCTAAA 1334
      |||
Db      1460 GGAATACCTCTAAA 1474
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; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118153
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118153

Query Match      13.6%; Score 182.2; DB 5; Length 1035;
Best Local Similarity 93.6%; Pred. No. 1.8e-36;
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 265
Db 187 TTTGTTTTTTTACTTTAAAGAACTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 246

Qy 266 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325
Db 247 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306

Qy 326 TAAATTGCGTATAGACGACAGAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 385
Db 307 TAAATTGCGTATAGACGACAGAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 366

Qy 386 TACACCAATTCGCAAAAGCTCAGA 408
Db 367 TACACCAATTCGCAAAAGGTAAGA 389

RESULT 12
US-10-027-632-118154
; Sequence 118154, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118153
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118153

Query Match      13.6%; Score 182.2; DB 6; Length 1035;
Best Local Similarity 93.6%; Pred. No. 1.8e-36;
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 265
Db 187 TTTGTTTTTTTACTTTAAAGAACTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 246

Qy 266 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325
Db 247 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306

Qy 326 TAAATTGCGTATAGACGACAGAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 385
Db 307 TAAATTGCGTATAGACGACAGAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 366

Qy 386 TACACCAATTCGCAAAAGCTCAGA 408
Db 367 TACACCAATTCGCAAAAGGTAAGA 389

RESULT 13
US-10-027-632-118153
; Sequence 118153, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118153
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118153

Query Match      13.6%; Score 182.2; DB 6; Length 1035;
Best Local Similarity 93.6%; Pred. No. 1.8e-36;
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 265
Db 187 TTTGTTTTTTTACTTTAAAGAACTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 246

Qy 266 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325
Db 247 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306

Qy 326 TAAATTGCGTATAGACGACAGAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 385
Db 307 TAAATTGCGTATAGACGACAGAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 366

Qy 386 TACACCAATTCGCAAAAGCTCAGA 408
Db 367 TACACCAATTCGCAAAAGGTAAGA 389

RESULT 14
US-10-027-632-118154
; Sequence 118154, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118154
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118154

Query Match      13.6%; Score 182.2; DB 5; Length 1035;
Best Local Similarity 93.6%; Pred. No. 1.8e-36;
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 265
Db 187 TTTGTTTTTTTACTTTAAAGAACTGGGATGGAATAATTGGATAAAATTTGCTGGGTGTCA 246
```

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
POLYMORPHISMS IN THE HUMAN GENOME  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 118154  
LENGTH: 1035  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-118154

Query Match 13.6%; Score 182.2; DB 6; Length 1035;  
Best Local Similarity 93.6%; Pred. No. 1.8e-36;  
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 206 TTTTTCATTCGATTATCAAAAACGCGGATGGATTAATTGGATAAAATTTGCTGGGTGCA 265  
DB 187 TTGTTTTTTTACTTTAAAGAACTGGGATGGATTAATTGGATAAAATTTGCTGGGTGCA 246  
QY 266 GAATATTACTAGTACCAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325  
DB 247 GAATATTACTAGTACCAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306  
QY 326 TAAATTGCGTATAGAGCAGAAAAGAACACTTCTTCATGTTATGAGTTGACTCATT 385  
DB 307 TAAATTGCGTATAGAGCAGAAAAGAACACTTCTTCATGTTATGAGTTGACTCATT 366  
QY 386 TACACCATTTGCAAGCTCAGA 408  
DB 367 TACACCATTTGCAAGCTAAGA 389

RESULT 15  
US-10-450-763-17284  
Sequence 17284, Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 17284  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIMILAR

LOCATION: (88)..(165)  
OTHER INFORMATION: 100% homologous to Homo sapiens interferon alpha/beta  
OTHER INFORMATION: receptor, accession number X60459, Smith-Waterman Score=122.  
US-10-450-763-17284  
Query Match 7.3%; Score 98.6; DB 9; Length 579;  
Best Local Similarity 96.2%; Pred. No. 7.7e-15;  
Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CTGCAGGATCTGCGCGGCTCCAGATGATGTCCTCTGGGGCGGACGACCCCTAG 60  
DB 62 CTGCTGGGATCTGCGCGGCTCCAGATGATGTCCTCTGGGGCGGACGACCCCTAG 121  
QY 61 TGCTCTGCTGCGCGGCTGGGCCCATGGGTGTTGTCGCGCAGCCGAGGTG 105  
DB 122 TGCTCTGCTGCGCGGCTGGGCCCATGGGTGTTGTCGCGCAGCCGAGGTG 166  
Search completed: January 18, 2006, 02:01:25  
Job time : 1204 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1343	100.0	1343	2	AAQ14239	Encodes s
2	1343	100.0	1343	2	AAQ30532	Sequence
3	1343	100.0	1343	2	AAQ49625	Human int
4	1338.2	99.6	1343	2	AAQ866457	Adn866457
5	1334	99.3	1755	2	AAQ14240	IFN-R ext
6	1334	99.3	1755	2	AAQ30533	Sequence
7	1334	99.3	1755	2	AAQ49624	Human int
8	1332.4	99.2	1755	2	AAQ866458	Human IFN
9	1330.8	99.1	2755	11	AD131792	Human CD
10	1330.8	99.1	2755	13	ADR66494	Human pr
11	1330.8	99.1	2755	13	ADR66152	Human pr
12	1330.8	99.1	2755	13	ADR38359	Human ly
13	1330.8	99.1	2755	14	ADW86762	Human in
14	1330.8	99.1	2784	2	AAQ11701	Human alp
15	1327.2	98.8	2017	3	AAF16297	Human pro
16	1326	98.7	2278	6	AA662251	cDNA sequ
17	1326	98.7	2827	13	ACF87579	Human SI
18	1318.6	98.2	6741	12	ADK23578	Human IF
19	1313.2	97.8	1512	14	ADV25069	INR1 T11

CC extracellular portion of the interferon-alpha and/or beta receptor. The  
 CC transmembrane and cytoplasmic domains of the native receptor have been  
 CC deleted to obtain a soluble, circulating form of the receptor.  
 CC Potentially immunogenic epitopes have thus been eliminated. See also  
 CC ARL4240  
 XX  
 SQ Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1343; DB 2; Length 1343;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTCGAGGATCTCGCGCGCTCCAGATGATGTCGTCCTCTCGGCGCAGCACCTAG 60  
 DB 1 CTCGAGGATCTCGCGCGCTCCAGATGATGTCGTCCTCTCGGCGCAGCACCTAG 60  
 QY 61 TGTCTGTCGCGTGGGCCATGGGTGTTCGCGAGCGGAGGTGGAAAAATCTAAAT 120  
 DB 61 TGTCTGTCGCGTGGGCCATGGGTGTTCGCGAGCGGAGGTGGAAAAATCTAAAT 120  
 QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 180  
 DB 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 180  
 QY 181 GCGATGAGTCTGTCGCGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
 DB 181 GCGATGAGTCTGTCGCGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
 QY 241 ATTGGAATAAATGTCGCGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTCAC 300  
 DB 241 ATTGGAATAAATGTCGCGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTCAC 300  
 QY 301 TCAAGCTGAATGTTTATGAAGAATAAATTAAGTATTAAGCAGAGCAAAAAAGAACACTT 360  
 DB 301 TCAAGCTGAATGTTTATGAAGAATAAATTAAGTATTAAGCAGAGCAAAAAAGAACACTT 360  
 QY 361 CTTTCATGATGAGTGTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
 DB 361 CTTTCATGATGAGTGTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
 QY 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTATACATCTCTCTGGAAACAAAAG 480  
 DB 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTATACATCTCTCTGGAAACAAAAG 480  
 QY 481 ATAGTGTTATGTCGCTTTCGATGTTTAAAGCTTTACATATAGTCTTATCTCGAAA 540  
 DB 481 ATAGTGTTATGTCGCTTTCGATGTTTAAAGCTTTACATATAGTCTTATCTCGAAA 540  
 QY 541 ACTCTTCAGGTGTAGAAAGAGGATGAAAATATTTATTCAGACATATAAATTTATAAAC 600  
 DB 541 ACTCTTCAGGTGTAGAAAGAGGATGAAAATATTTATTCAGACATATAAATTTATAAAC 600  
 QY 601 TCTCACAGAGACTACTTATTTGCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAA 660  
 DB 601 TCTCACAGAGACTACTTATTTGCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAA 660  
 QY 661 TTGCTGTCTATAGTCCAGTACATTTATTAAGCCACAGTTGAAATGAACTACCTCCAC 720  
 DB 661 TTGCTGTCTATAGTCCAGTACATTTATTAAGCCACAGTTGAAATGAACTACCTCCAC 720  
 QY 721 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTTATACAT 780  
 DB 721 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTTATACAT 780  
 QY 781 ATGCAACATGACTTTTCAAGTTCAGTGGCTTCCACGCTTTTAAAAAGGAATCTGGAA 840  
 DB 781 ATGCAACATGACTTTTCAAGTTCAGTGGCTTCCACGCTTTTAAAAAGGAATCTGGAA 840  
 QY 841 ACCATTGTATTAATGAAACAAATACCTGCTGGAATGTCMAAATCACTACCCAGTGTG 900  
 DB 841 ACCATTGTATTAATGAAACAAATACCTGCTGGAATGTCMAAATCACTACCCAGTGTG 900  
 QY 901 TCTTTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960

DB 901 TCTTTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960  
 QY 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGTATCTGAAATACAAGCTTTCC 1020  
 DB 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGTATCTGAAATACAAGCTTTCC 1020  
 QY 1021 TACTTCTCCAGTCTTTTAACATTTAGATCCCTTAGTGATTCATTCCCATATCTATATCGGTG 1080  
 DB 1021 TACTTCTCCAGTCTTTTAACATTTAGATCCCTTAGTGATTCATTCCCATATCTATATCGGTG 1080  
 QY 1081 CTCAAAAACAGTCTGAAAAACACGCTGTGATCCAGGATTCACCTGATTTATGAAATTA 1140  
 DB 1081 CTCAAAAACAGTCTGAAAAACACGCTGTGATCCAGGATTCACCTGATTTATGAAATTA 1140  
 QY 1141 TTTTGGGAAAAACACTTCAAAATGCTGAGAGAAAAATTCGAGAAAAAACTGATGTTA 1200  
 DB 1141 TTTTGGGAAAAACACTTCAAAATGCTGAGAGAAAAATTCGAGAAAAAACTGATGTTA 1200  
 QY 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGAGCACACCATGG 1260  
 DB 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGAGCACACCATGG 1260  
 QY 1261 ATGAAAAGCTGAATAAAAACAGCTGTTTTTTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
 DB 1261 ATGAAAAGCTGAATAAAAACAGCTGTTTTTTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
 QY 1321 GAAATACCTCTAAATGAGGTACC 1343  
 DB 1321 GAAATACCTCTAAATGAGGTACC 1343  
 RESULT 2  
 AAQ30532  
 ID AAQ30532 standard; DNA; 1343 BP.  
 XX  
 AC AAQ30532;  
 DT 25-MAR-2003 (revised)  
 DT 31-MAR-1993 (first entry)  
 XX  
 DE Sequence encoding a soluble form of the interferon (IFN) receptor with a  
 DE high affinity for IFN-alpha and -beta.  
 XX  
 KW Interferon receptor; alpha-interferon; beta-interferon; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 27..1337  
 FT /\*tag= a  
 XX  
 FN W09218626-A1.  
 XX  
 PD 29-OCT-1992.  
 XX  
 PF 17-APR-1991; 91WO-FR000318.  
 XX  
 PR 17-APR-1991; 91WO-FR000318.  
 XX  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.  
 XX  
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
 PI Uze G;  
 XX  
 DR WPI; 1992-382110/46.  
 DR P-PSDB; AAR28495.  
 XX  
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
 PT useful as immunosuppressants, for treating autoimmune diseases and  
 PT transplant rejection.  
 XX  
 PS Claim 10; Fig 1; 58pp; English.

XX DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
 CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
 CC primers and cloned cDNA as template. For example, bacteriophage lambda  
 CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
 CC receptor (AA030533), was incubated with oligos AA030534 and AA030535.  
 CC AA028496 represents the complete receptor. AA028495 lacks the  
 CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
 CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
 CC diseases and graft rejection. They lack the toxic side-effects of known  
 CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX

Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T; 0 U; 0 Other;

Query Match 100.0%; Score 1343; DB 2; Length 1343;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTG CAGGATCTGGGGCTCCAGATGATGGTGGTCTCTGGGGCGGACCCCTAG 60  
 Db 1 CTG CAGGATCTGGGGCTCCAGATGATGGTGGTCTCTGGGGCGGACCCCTAG 60

Qy 61 TGCTCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
 Db 61 TGCTCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120

Qy 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGTGGGAACAGGA 180  
 Db 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGTGGGAACAGGA 180

Qy 181 GCGATGATCTGTGGGGAATGCACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
 Db 181 GCGATGATCTGTGGGGAATGCACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240

Qy 241 ATTGGATAAATTTGTCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTCTTCAC 300  
 Db 241 ATTGGATAAATTTGTCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTCTTCAC 300

Qy 301 TCAAGCTCAATGTTTATCAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360  
 Db 301 TCAAGCTCAATGTTTATCAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360

Qy 361 CTTTCATGTTGAGGTGCTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGCTCCAG 420  
 Db 361 CTTTCATGTTGAGGTGCTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGCTCCAG 420

Qy 421 AAGTACATTTAGAACTGAAGTAAGGCAATAGTATACATCTCTCTCTGGAAACAAAG 480  
 Db 421 AAGTACATTTAGAACTGAAGTAAGGCAATAGTATACATCTCTCTCTGGAAACAAAG 480

Qy 481 ATAGTGTATGTTGGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTATCTCGAAAA 540  
 Db 481 ATAGTGTATGTTGGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTATCTCGAAAA 540

Qy 541 ACTCTTCAGGTGTAGAAGAAAGATTGAAATATTTATTTCCAGACATAAAATTTATAAC 600  
 Db 541 ACTCTTCAGGTGTAGAAGAAAGATTGAAATATTTATTTCCAGACATAAAATTTATAAC 600

Qy 601 TCTCACCAGAGACTACTTATTGCTCTAAAGTTTAAAGCAGCACTACTTACGTCATGAAAA 660  
 Db 601 TCTCACCAGAGACTACTTATTGCTCTAAAGTTTAAAGCAGCACTACTTACGTCATGAAAA 660

Qy 661 TTGGTGTCTATAGTCCAGTACATTTCTATAAGATTAAGCAGCACTACTTACGTCATGAAAA 720  
 Db 661 TTGGTGTCTATAGTCCAGTACATTTCTATAAGATTAAGCAGCACTACTTACGTCATGAAAA 720

Qy 721 CAGAAATATAGAAGTCCAGTCCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780  
 Db 721 CAGAAATATAGAAGTCCAGTCCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780

Qy 781 ATGCAAAATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840  
 Db 781 ATGCAAAATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840

Db 781 ATGCAAAATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840  
 Qy 841 ACCATTTGTATAAATGAAAACAATACTGCTGTGAAAAATGTCAAACTACCCAGTGTG 900  
 Db 841 ACCATTTGTATAAATGAAAACAATACTGCTGTGAAAAATGTCAAACTACCCAGTGTG 900  
 Qy 901 TCTTCTCTCAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCGGGTCAAGCACTCTGATG 960  
 Db 901 TCTTCTCTCAAAAGCTTTTCCAAAAAGAAATTTACCTTCTCGGGTCAAGCACTCTGATG 960  
 Qy 961 GAAATAACACATCTTTTGTGCTGAAGAGATAAAGTTTGTATCTGAAATACAAGCTTTCC 1020  
 Db 961 GAAATAACACATCTTTTGTGCTGAAGAGATAAAGTTTGTATCTGAAATACAAGCTTTCC 1020  
 Qy 1021 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGTGATTCATTCATATCTATATCGGTG 1080  
 Db 1021 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGTGATTCATTCATATCTATATCGGTG 1080  
 Qy 1081 CTCCAAAACAGTCTGGAACACGCGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1140  
 Db 1081 CTCCAAAACAGTCTGGAACACGCGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1140  
 Qy 1141 TTTTTCGGAAAAACACTTTCAAATGCTGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
 Db 1141 TTTTTCGGAAAAACACTTTCAAATGCTGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
 Qy 1201 CAGTTCCTAAATTTGAAACCACTGATCTGATATTTGTGAAAGCCAGAGACACACCATGG 1260  
 Db 1201 CAGTTCCTAAATTTGAAACCACTGATCTGATATTTGTGAAAGCCAGAGACACACCATGG 1260  
 Qy 1261 ATGAAAAGCTGAAATTAAGAGCTGTTTTTGTAGTGGCTGTATGTGAGAAAAACAAACAG 1320  
 Db 1261 ATGAAAAGCTGAAATTAAGAGCTGTTTTTGTAGTGGCTGTATGTGAGAAAAACAAACAG 1320  
 Qy 1321 GAAATACCTCTAAATGAGGTACC 1343  
 Db 1321 GAAATACCTCTAAATGAGGTACC 1343

RESULT 3  
 AA049625  
 ID AA049625 standard; DNA; 1343 BP.  
 XX  
 AC AA049625;  
 XX  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 20-APR-1994 (first entry)  
 XX  
 DE Human interferon receptor extracellular domain coding sequence.  
 XX  
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; interferon-alpha-beta; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 27..1337  
 FT /\*tag= a  
 FT /note= "encodes extra cellular domain of IFN-R"  
 XX  
 PN EP563487-Al.  
 XX  
 XX  
 PD 06-OCT-1993.  
 XX  
 PF 31-MAR-1992; 92EP-00400902.  
 XX  
 PR 31-MAR-1992; 92EP-00400902.  
 XX  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 XX  
 PI Benoit P, Meyer F, Maguire D, Plavec I, Tovey MG;



PI	Tovey MG, Benizri EJ;	
XX	WPI; 1995-131187/17.	
DR	P-PSDB; AAR71723.	
XX		
XX	Compsn. of monoclonal antibodies against interferon receptor - useful as	
PT	immuno-modulator, eg. for treating AIDS.	
XX		
XX	Disclosure; Fig 2A-2B; 105pp; English.	
PS		
XX	DNA encoding the extracellular domain of the human IFN class I receptor	
CC	is given in AA086457. Monoclonal antibodies were raised against the	
CC	recombinant soluble form of the encoded protein (AAR71723) expressed in	
CC	either E. coli or COS cell hosts. (Updated on 25-MAR-2003 to correct PN	
CC	field.)	
XX		
XX	Sequence 1343 BP; 449 A; 257 C; 261 G; 376 T; 0 U; 0 Other;	
SQ		
	Query Match 99.6%; Score 1338.2; DB 2; Length 1343;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 1340; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 CTGCAGGATCTGGCGGCTCCAGATGATGCTCTCTCTGGGCGGACGACCTTAG 60	
Db	1 CTGCAGGATCTGGCGGCTCCAGATGATGCTCTCTCTGGGCGGACGACCTTAG 60	
Qy	61 TGCTCTGCTGGCGGCTCCAGATGATGCTCTCTCTGGGCGGACGACCTTAG 120	
Db	61 TGCTCTGCTGGCGGCTCCAGATGATGCTCTCTCTGGGCGGACGACCTTAG 120	
Qy	121 CTCTCTCAAAAAGTAGAGTGCACATCATAGATGACACTTATCTGAGGTGGACAGGA 180	
Db	121 CTCTCTCAAAAAGTAGAGTGCACATCATAGATGACACTTATCTGAGGTGGACAGGA 180	
Qy	181 GCGATGACTCTCGGGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240	
Db	181 GCGATGACTCTCGGGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240	
Qy	241 ATTGGATAAAATTTGCTGGGTGTCAGATATTTACTAGTACCAATGCACTTTTCTTCCAC 300	
Db	241 ATTGGATAAAATTTGCTGGGTGTCAGATATTTACTAGTACCAATGCACTTTTCTTCCAC 300	
Qy	301 TCAAGCTGAATTTTATGAGAAATTAATTTGCGTATAGGACGAGAAAGAAACACTT 360	
Db	301 TCAAGCTGAATTTTATGAGAAATTAATTTGCGTATAGGACGAGAAAGAAACACTT 360	
Qy	361 CTTCATGTATGAGTGCACATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420	
Db	361 CTTCATGTATGAGTGCACATTTACACCAATTTGCAAGCTCAGATTGGTCTCCAG 420	
Qy	421 AAGTACATTTAGAGCTGAAGTAAAGCAATAGTATACATCTCTCTCTGGAACAAAG 480	
Db	421 AAGTACATTTAGAGCTGAAGTAAAGCAATAGTATACATCTCTCTCTGGAACAAAG 480	
Qy	481 ATAGTGTATGCGCTTTGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGAAA 540	
Db	481 ATAGTGTATGCGCTTTGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGAAA 540	
Qy	541 ACTCTTCAGGTGAGAGAGGATGAAAATATTATTATTCAGACATATAAATTTATAAC 600	
Db	541 ACTCTTCAGGTGAGAGAGGATGAAAATATTATTATTCAGACATATAAATTTATAAC 600	
Qy	601 TCTCACCAGACTACTTATTGCTTAAAGTTAAAGCAGCACTACTTACGTCATGGA 660	
Db	601 TCTCACCAGACTACTTATTGCTTAAAGTTAAAGCAGCACTACTTACGTCATGGA 660	
Qy	661 TTGGTGTCTATAGTCCAGTACATTTGATAAAGCAGCACTACTTACGTCATGGA 720	
Db	661 TTGGTGTCTATAGTCCAGTACATTTGATAAAGCAGCACTACTTACGTCATGGA 720	
Qy	721 CAGAAAATATAGAGTTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780	
Db	721 CAGAAAATATAGAGTTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780	

RESULT 5

AAQ14240

ID AAQ14240 standard; DNA; 1755 BP.

XX AC AAQ14240;

XX DT 16-JAN-1992 (first entry)

XX DE Encodes complete interferon-alpha/beta receptor.

XX KW IFN; autoimmune disease; graft rejection; histocompatibility; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

XX FT 27..1700

XX FT /\*tag= a

XX PN FR2657881-A.

XX PD 09-AUG-1991.

XX PF 05-FEB-1990; 90FR-00001298.

XX PR 05-FEB-1990; 90FR-00001298.

XX PA (EUBI-) LAB EURO BIOTECHNO.

XX PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG;

XX PI Uze G;

XX



DR WPI; 1991-319778/44.  
XX P-PSDB; AAR14488.  
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
PT used to treat e.g. lupus erythematosus, Behcet's disease, aaplastic  
PT anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX  
PS Disclosure; Page 47; 52pp; French.  
XX  
CC The protein encoded by this sequence corresponds to the complete  
CC interferon-alpha and/or beta receptor. The invention covers derivatives  
CC of the receptor obtained by deleting the transmembrane and cytoplasmic  
CC domains of the native receptor or by substitution. See also AAQ14239  
XX  
SQ Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T; 0 U; 0 Other;  
  
Query Match 99.38; Score 1334; DB 2; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CTG CAGGAGATCTGGCGGGCTCCAGATGATGGTGCCTCTGGGGCGGACGACCCCTAG 60  
DB |||||  
1 CTG CAGGAGATCTGGCGGGCTCCAGATGATGGTGCCTCTGGGGCGGACGACCCCTAG 60  
||  
QY 61 TGCTGTCGCGCGTGGGCCCATGGGTGTGTCGCGAGCCGAGGTGGAAAAATCTAAAT 120  
DB |||||  
61 TGCTGTCGCGCGTGGGCCCATGGGTGTGTCGCGAGCCGAGGTGGAAAAATCTAAAT 120  
||  
QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGAACGGA 180  
DB |||||  
121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGAACGGA 180  
||  
QY 181 GCGATGAGTCTGTCGCGGAATGTGACTTTTTCATTCGATATCAAAAACTGGGATGGATA 240  
DB |||||  
181 GCGATGAGTCTGTCGCGGAATGTGACTTTTTCATTCGATATCAAAAACTGGGATGGATA 240  
||  
QY 241 ATTGGATAAAATTTGTCGCGGTGTCAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC 300  
DB |||||  
241 ATTGGATAAAATTTGTCGCGGTGTCAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC 300  
||  
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGTTATAGAGCGAAAAAGAAACACTT 360  
DB |||||  
301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGTTATAGAGCGAAAAAGAAACACTT 360  
||  
QY 361 CTTCATGATGAGTGTGACTCATTTACACCATTTCCGAAAGCTCAGATTGCTCCAG 420  
DB |||||  
361 CTTCATGATGAGTGTGACTCATTTACACCATTTCCGAAAGCTCAGATTGCTCCAG 420  
||  
QY 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480  
DB |||||  
421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480  
||  
QY 481 ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAA 540  
DB |||||  
481 ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAA 540  
||  
QY 541 ACTCTCAGGTGTAGAAGAAAGGATGAAAATTTTATCCAGACATAAAATTTATAAC 600  
DB |||||  
541 ACTCTCAGGTGTAGAAGAAAGGATGAAAATTTTATCCAGACATAAAATTTATAAC 600  
||  
QY 601 TCTCACCAGAGACTACTTATGTCCTAAAAGTTAAAGCAGCAGCTACTTTACGTCATGGA 660  
DB |||||  
601 TCTCACCAGAGACTACTTATGTCCTAAAAGTTAAAGCAGCAGCTACTTTACGTCATGGA 660  
||  
QY 661 TTGGTGTCTATAGTCCAGTACATTTGTATTAAGACCAAGTTGAAAATGAATCTACCTCCAC 720  
DB |||||  
661 TTGGTGTCTATAGTCCAGTACATTTGTATTAAGACCAAGTTGAAAATGAATCTACCTCCAC 720  
||  
QY 721 CAGAAATATAGAGTGCAGTCTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
DB |||||  
721 CAGAAATATAGAGTGCAGTCTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
||  
QY 781 ATGCAAAACATGACCTTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840

DB |||||  
781 ATGCAAAACATGACCTTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCTGGAA 840  
||  
QY 841 ACCATTGTATTAATGGAACAAATACCTGACTGTGAAAATGTCAAAATCTACCCAGTGTG 900  
DB |||||  
841 ACCATTGTATTAATGGAACAAATACCTGACTGTGAAAATGTCAAAATCTACCCAGTGTG 900  
||  
QY 901 TCTTTCTCAAAACAGTTCCTTCCAAAAAGGAATTTACCTTCTCCGCGTACAGCATCTGATG 960  
DB |||||  
901 TCTTTCTCAAAACAGTTCCTTCCAAAAAGGAATTTACCTTCTCCGCGTACAGCATCTGATG 960  
||  
QY 961 GAAATTAACATCTTTTGGTCTGAAGAGATAAAGTTTGAATCTGAAATCAAGCTTTCC 1020  
DB |||||  
961 GAAATTAACATCTTTTGGTCTGAAGAGATAAAGTTTGAATCTGAAATCAAGCTTTCC 1020  
||  
QY 1021 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGTGATTCATTCATCTATATCGGTG 1080  
DB |||||  
1021 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGTGATTCATTCATCTATATCGGTG 1080  
||  
QY 1081 CTCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1140  
DB |||||  
1081 CTCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1140  
||  
QY 1141 TTTTGGGAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
DB |||||  
1141 TTTTGGGAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
||  
QY 1201 CAGTTCCTAATTTGAAACCACTGCTGATATTTGTGGAAGCCAGACACACCATGG 1260  
DB |||||  
1201 CAGTTCCTAATTTGAAACCACTGCTGATATTTGTGGAAGCCAGACACACCATGG 1260  
||  
QY 1261 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
DB |||||  
1261 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
||  
QY 1321 GAAATACCTCTAAA 1334  
DB |||||  
1321 GAAATACCTCTAAA 1334  
||  
RESULT 6  
AAQ30533  
ID AAQ30533 standard; DNA; 1755 BP.  
XX  
AC AAQ30533;  
XX  
XX 25-MAR-2003 (revised)  
DT 31-MAR-1993 (first entry)  
XX  
DE Sequence encoding a soluble form of the interferon (IFN) receptor with a  
DE high affinity for IFN-alpha and -beta.  
XX  
XX Interferon receptor; alpha-interferon; beta-interferon; ss.  
XX  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
CDS 27..1700  
FT /\*tag= a  
XX  
XX WO9218626-A1.  
PN  
XX  
PD 29-OCT-1992.  
XX  
PF 17-APR-1991; 91WO-FR000318.  
XX  
PR 17-APR-1991; 91WO-FR000318.  
XX  
XX (EUBI-) LAB EURO BIOTECHNOLOGIE.  
XX  
XX Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
PI Uze G;  
XX

DR	WPI; 1992-382110/46.	Db	661	TTGGTGTCTATAGTCCAGTACATTTGTATATAAGACCACAGTTGAAATGAACCTACCTCCAC	720
DR	P-PSDB; AAR28496.	Qy	721	CAGAAAATATAGAAAGTCAAGTGTCCAAATCAGAACTATGTTCTTTAAATGGATATATACAT	780
PT	Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -	Db	721	CAGAAAATATAGAAAGTCAAGTGTCCAAATCAGAACTATGTTCTTTAAATGGATATATACAT	780
PT	useful as immunosuppressants, for treating auto-immune diseases and	Qy	781	ATGCAAAACATGACCTTTCAAGTTCCAGTGGCTCCAGCGCTTTTAAAGAGGAATCCTGAA	840
PT	transplant rejection.	Db	781	ATGCAAAACATGACCTTTCAAGTTCCAGTGGCTCCAGCGCTTTTAAAGAGGAATCCTGAA	840
PS	Claim 10; Fig 2; 58pp; English.	Qy	841	ACCAATTTGTATAATGGAAACAAATACCTGACTGTGAAAAATGTCAAACTACCCAGTGTG	900
XX	DNA encoding the water-soluble polypeptide with a high affinity for IFN-	Db	841	ACCAATTTGTATAATGGAAACAAATACCTGACTGTGAAAAATGTCAAACTACCCAGTGTG	900
CC	alpha and -beta is isolated by PCR, using appropriate oligonucleotides as	Qy	901	TCCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCCCGGTACAGCATCTGATG	960
CC	primers and cloned cDNA as template. For example, bacteriophage lambda	Db	901	TCCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCCCGGTACAGCATCTGATG	960
CC	ZAP, containing the entire coding sequence of the IFN-alpha and -beta	Qy	961	GAATAACACATCTTTTGGTCTGAAAGAGATAAAGTTTGATACCTGAAATCAAGCTTTCC	1020
CC	receptor (AA030533), was incubated with oligos AA030534 and AA030535.	Db	961	GAATAACACATCTTTTGGTCTGAAAGAGATAAAGTTTGATACCTGAAATCAAGCTTTCC	1020
CC	AA030535 represents the complete receptor. AAR28495 lacks the	Qy	1021	TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGAATTCATTCATATCTATATCGGTG	1080
CC	transmembrane and cytoplasmic domains. Both forms bind IFN in the same	Db	1021	TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGAATTCATTCATATCTATATCGGTG	1080
CC	way as antibodies so are immunosuppressants e.g. for treating autoimmune	Qy	1081	CTCAAAACAGTCTGGAACACACGCTGTGATCCAGGATATCCACTGATTTATGAATTA	1140
CC	diseases and graft rejection. They lack the toxic side-effects of known	Db	1081	CTCAAAACAGTCTGGAACACACGCTGTGATCCAGGATATCCACTGATTTATGAATTA	1140
CC	immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct	Qy	1141	TTTTTGGGAAAAACACTTCAAAATCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA	1200
CC	PN field.)	Db	1141	TTTTTGGGAAAAACACTTCAAAATCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA	1200
XX	Sequence 1755 BP; 593 A; 325 C; 333 G; 504 T; 0 U; 0 Other;	Qy	1201	CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTAAGCCAGACACACACCATGG	1260
XX	Query Match .99.3%; Score 1334; DB 2; Length 1755;	Db	1201	CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTAAGCCAGACACACACCATGG	1260
XX	Best Local Similarity 100.0%; Pred. No. 0;	Qy	1261	ATGAAAAGCTGAAATAAAGAGAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAAACAACAG	1320
XX	Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1261	ATGAAAAGCTGAAATAAAGAGAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAAACAACAG	1320
Qy	1 CTGAGGAGATCTGCGGGCTCCAGATGATGGTCTCTCTGGGGCGGACGCCCTAG 60	Qy	1321	GAATACCTCTAAA 1334	
Db	1 CTGAGGAGATCTGCGGGCTCCAGATGATGGTCTCTCTGGGGCGGACGCCCTAG 60	Db	1321	GAATACCTCTAAA 1334	
Qy	61 TGCTCGTCCGCGGCGCCATGGTGTGTCGAGCGCGAGGTGGAATAATCTAAAT 120	RESULT 7			
Db	61 TGCTCGTCCGCGGCGCCATGGTGTGTCGAGCGCGAGGTGGAATAATCTAAAT 120	AAQ49624			
Qy	121 CTCCTCAAAAAGTAGAGTCCACATCATAGATGACACTTTTATCTGAGGTGGACACAGA 180	ID AAQ49624 standard; DNA; 1755 BP.			
Db	121 CTCCTCAAAAAGTAGAGTCCACATCATAGATGACACTTTTATCTGAGGTGGACACAGA 180	XX AAQ49624;			
Qy	181 GCGATGAGTCTGCGGGAATGACTTTTTCATTCGATTTATCAAAAACTGGGATGGATA 240	AC AC			
Db	181 GCGATGAGTCTGCGGGAATGACTTTTTCATTCGATTTATCAAAAACTGGGATGGATA 240	XX AC			
Qy	241 ATTGGATAAAATTTGTCGGGTGTCGAAATATATCTAGTACCAATGCACTTTTCTTCAC 300	DT 25-MAR-2003 (revised)			
Db	241 ATTGGATAAAATTTGTCGGGTGTCGAAATATATCTAGTACCAATGCACTTTTCTTCAC 300	DT 20-APR-1994 (first entry)			
Qy	301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGGTATAAGAGCAGAAAAACACTT 360	XX Human interferon receptor coding sequence.			
Db	301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGGTATAAGAGCAGAAAAACACTT 360	XX IFN-R; extracellular domain; monoclonal antibody; viral infection;			
Qy	361 CTTTCATGATGAGGTGACTCAATTTACCAATTTCCAAAGCTCAGATTGGTCTCCAG 420	XX cell proliferation; allograft rejection; systemic lupus erythematosus;			
Db	361 CTTTCATGATGAGGTGACTCAATTTACCAATTTCCAAAGCTCAGATTGGTCTCCAG 420	XX psoriasis; multiple sclerosis; Bence's Disease; aplastic anaemia;			
Qy	421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480	XX immunodeficiency; measles virus; interferon-alpha-beta; ss.			
Db	421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480	XX Homo sapiens.			
Qy	481 ATAGTGTATCTGGCTTTGGATGTTTAAAGCTTACATATAGCTTACTTATCTGAAAA 540	XX Key Location/Qualifiers			
Db	481 ATAGTGTATCTGGCTTTGGATGTTTAAAGCTTACATATAGCTTACTTATCTGAAAA 540	XX CDS 27..1700			
Qy	541 ACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTATTTCCAGACATAAAATTTATAAC 600	XX Key Location/Qualifiers			
Db	541 ACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTATTTCCAGACATAAAATTTATAAC 600	XX CDS 27..1700			
Qy	601 TCTCACAGAGACTATTTATTTCTTAAAGTTAAAGCAGCACTACTTACGTCATGAAAA 660	XX Key Location/Qualifiers			
Db	601 TCTCACAGAGACTATTTATTTCTTAAAGTTAAAGCAGCACTACTTACGTCATGAAAA 660	XX CDS 27..1700			
Qy	661 TTGGTGTCTATAGTCCAGTACATTTGTATATAAGACCACAGTTGAAATGAACCTACCTCCAC 720	XX Key Location/Qualifiers			
Db	661 TTGGTGTCTATAGTCCAGTACATTTGTATATAAGACCACAGTTGAAATGAACCTACCTCCAC 720	XX CDS 27..1700			



[illegible]

XX 09-FEB-1998; 98US-00023655.  
XX  
PR 09-FEB-1998; 98US-00023655.  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Cocks BG, Stuart SG, Seilhamer JJ;  
XX WPI; 2003-895307/82.  
XX  
PT A composition comprising a plurality of cDNAs, useful for detecting  
PT altered expression of genes in an immunological response or for  
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
PT or osteoarthritis.  
XX  
PS Claim 1; SEQ ID NO 1118; 50pp; English.  
XX  
CC The invention relates to a composition comprising a plurality of cDNAs  
CC for detecting the altered expression of genes in an immunological  
CC response. The invention also relates to a method of diagnosing or  
CC monitoring the treatment of an immunopathological condition in a sample,  
CC comprising obtaining nucleic acids from a sample, contacting the nucleic  
CC acids of the sample with an array comprising the plurality of cDNAs under  
CC conditions to form one or more hybridisation complexes, detecting the  
CC hybridisation complexes and comparing the levels of the detected  
CC hybridisation complexes with the level of hybridisation complexes  
CC detected in a non-diseased sample, where an altered level of the detected  
CC hybridisation complexes correlates with the presence of an  
CC immunopathological condition. Also disclosed are an expression profile  
CC comprising a microarray and a plurality of detectable complexes and a  
CC method for identifying a plurality of polynucleotide probes. The cDNAs  
CC are useful as hybridisable array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray can be used in  
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,  
CC ulcerative colitis, hyperosinophilia, irritable bowel syndrome,  
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in  
CC identifying agents for the treatment of the diseases. The microarray may  
CC also be used in drug discovery and development, toxicological and  
CC carcinogenicity studies, forensics or pharmacogenomics. The composition  
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or  
CC genomic fragments. This sequence represents a human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification but was obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 11; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCGAGGATCTCGGCGGCTCCAGATGATGTCCTCTGGGCGGACGCCCTAG 60  
DB 53 CTGGTGGGATCTCGGCGGCTCCAGATGATGTCCTCTGGGCGGACGCCCTAG 112  
QY 61 TGCCTCTCGCGCTGGGCGGCTGGTGTGTCGCGAGCCGCGAGTGGAAAAATCTAAAT 120  
DB 113 TGCCTCTCGCGCTGGGCGGCTGGTGTGTCGCGAGCCGCGAGTGGAAAAATCTAAAT 172  
QY 121 CTCTCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTCGAGGTGGAAACAGGA 180  
DB 173 CTCTCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTCGAGGTGGAAACAGGA 232  
QY 181 GCGATGAGTCTGCGGGAATGTGACCTTTTTCATTCGATATCAAAAAAATCTGGGATGATA 240  
DB 233 GCGATGAGTCTGCGGGAATGTGACCTTTTTCATTCGATATCAAAAAAATCTGGGATGATA 292  
QY 241 ATTGGATAAATGTCCTGGGTGTGAGAAATTAATAGTACCAATGCACTTTCTTCAC 300  
DB 293 ATTGGATAAATGTCCTGGGTGTGAGAAATTAATAGTACCAATGCACTTTCTTCAC 352  
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGGGTATGAAGCAGAAAAACACACTT 360

DB 353 TCAAGCTGAATGTTTATGAAGAAATTAATTTGGTATGAAGCAGAAAAAAGAAACACTT 412  
QY 361 CTTTCATGTTATGAGGTGTGACTCATTTACACCACTTTTCGAAAGCTCAGATTTGGTCTCCAG 420  
DB 413 CTTTCATGTTATGAGGTGTGACTCATTTACACCACTTTTCGAAAGCTCAGATTTGGTCTCCAG 472  
QY 421 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 480  
DB 473 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 532  
QY 481 ATAGTGTATGTTGGGCTTTTGGATGGTTTAAAGCTTTTACATATAGCTTTACTTTATCTGGAATA 540  
DB 533 ATAGTGTATGTTGGGCTTTTGGATGGTTTAAAGCTTTTACATATAGCTTTACTTTATCTGGAATA 592  
QY 541 ACTCTTCAGGTGTAGAAAGAGGATTTGAAAAATATTTATTTCCAGACATAAAATTTATAAAC 600  
DB 593 ACTCTTCAGGTGTAGAAAGAGGATTTGAAAAATATTTATTTCCAGACATAAAATTTATAAAC 652  
QY 601 TCTCACCCAGAGACTACTTATTTGCTAAAAAGTTAAAGCAGCAGCTACTTTACGTCATGGAATA 660  
DB 653 TCTCACCCAGAGACTACTTATTTGCTAAAAAGTTAAAGCAGCAGCTACTTTACGTCATGGAATA 712  
QY 661 TTGGTGTCTATAGTCCAGTACATTTGTATTAAGACCAACAGTTGAAAAATGAACCTACCTCCAC 720  
DB 713 TTGGTGTCTATAGTCCAGTACATTTGTATTAAGACCAACAGTTGAAAAATGAACCTACCTCCAC 772  
QY 721 CAGAAAAATATAGAAAGTCAAGTGTCCAAAATCAGAACTATGTTCTTTAAATGGGATTTACAT 780  
DB 773 CAGAAAAATATAGAAAGTCAAGTGTCCAAAATCAGAACTATGTTCTTTAAATGGGATTTACAT 832  
QY 781 ATGCAAAACATGACCTTTTCAAGTTCAGTGTGCTCCAGCCTTTTAAAAAGGAATCTCTGGAA 840  
DB 833 ATGCAAAACATGACCTTTTCAAGTTCAGTGTGCTCCAGCCTTTTAAAAAGGAATCTCTGGAA 892  
QY 841 ACCATTTGTATAAATGAAAAACAAATACCTGACTGTGAAAAATGTCAAAACTACCCAGTGTG 900  
DB 893 ACCATTTGTATAAATGAAAAACAAATACCTGACTGTGAAAAATGTCAAAACTACCCAGTGTG 952  
QY 901 TCTTTCTCAAAACGTTTTCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960  
DB 953 TCTTTCTCAAAACGTTTTCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 1012  
QY 961 GAAATAACACATCTTTTTCGCTCTGAAGAGATAAAGTTTGATACCTGAAATAACAAGCTTTCC 1020  
DB 1013 GAAATAACACATCTTTTTCGCTCTGAAGAGATAAAGTTTGATACCTGAAATAACAAGCTTTCC 1072  
QY 1021 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1080  
DB 1073 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1132  
QY 1081 CTCAAAAACAGTCTGGAACACAGCCTGTGATCCAGGATTTACCATGATTTTATGAAATTA 1140  
DB 1133 CTCAAAAACAGTCTGGAACACAGCCTGTGATCCAGGATTTATCCCATGATTTATGAAATTA 1192  
QY 1141 TTTTTCGGGAAACACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
DB 1193 TTTTTCGGGAAACACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252  
QY 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTGAAGCCAGAGACACACCATGG 1260  
DB 1253 CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTGAAGCCAGAGACACACCATGG 1312  
QY 1261 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGAACCTGTATGTGAGAAAAACAAACAG 1320  
DB 1313 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGAACCTGTATGTGAGAAAAACAAACAG 1372  
QY 1321 GAAATACCTCTAAA 1334  
DB 1373 GAAATACCTCTAAA 1386

AD66494	Query Match	99.1%;	Score 1330.8;	DB 13;	Length 2755;
ID	AD66494 standard; DNA; 2755 BP.	Best Local Similarity	99.9%;	Pred. No. 0;	
XX	AC	Matches 1332;	Conservative	0;	Mismatches
XX	AC	2;	Indels	0;	Gaps
XX	DT	02-DEC-2004	(first entry)		
XX	DE	Human prostatic carcinoma derived DNA SEQ ID 6 #3.			
XX	KW	human; cytostatic; diagnosis; prostatic cancer;			
XX	KW	differential expression analysis; ds.			
XX	OS	Homo sapiens.			
XX	FN	WO2004076614-A2.			
XX	PD	10-SEP-2004.			
XX	PF	22-FEB-2004; 2004WO-DE000433.			
XX	PR	27-FEB-2003; 2003DE-01009985.			
XX	PR	14-MAY-2003; 2003DE-01022134.			
XX	PA	(HINZ/) HINZMANN B.			
XX	PA	(DAHL/) DAHL E.			
XX	PA	(ROSE/) ROSENTHAL A.			
XX	PA	(HERM/) HERMANN K.			
XX	PA	(PILA/) PILARSKY C.			
XX	PI	Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;			
XX	PI	Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;			
XX	PI	Xinzhong L, Staub E;			
XX	DR	WPI; 2004-653386/63.			
XX	XX	New nucleic acids, and encoded proteins, from prostatic cancer tissue,			
XX	PT	useful for diagnosis, treatment and in screening for specific binding			
XX	PT	agents.			
XX	XX	Claim 1; Page 1087; 1607pp; German.			
XX	PS	This invention describes novel cytostatic polynucleotide and polypeptide			
XX	CC	sequences which can be used in a method for diagnosing prostatic cancer			
XX	CC	or the risk of developing prostatic cancer. Diagnosis is based on			
XX	CC	determining over transcription or over expression of the sequences in			
XX	CC	prostatic tissue. Screening for inhibitors of the sequences or detection			
XX	CC	substances involves a binding assay, any compounds that bind are			
XX	CC	selected, optionally after deconvolution of mixtures. Detection of a			
XX	CC	predetermined minimum level of the reporter indicates the presence of			
XX	CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,			
XX	CC	short-interfering RNA or ribozymes; an organic molecule of molecular			
XX	CC	weight below 5000, preferably 300, that binds to the polypeptide; an			
XX	CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the			
XX	CC	polypeptide, preferably humanised or human; an anti-idiotype, non-human			
XX	CC	(monoclonal) antibody directed against Ab or any of the above derivatised			
XX	CC	with a reporter group, cell toxin, immunostimulatory molecules and/or			
XX	CC	radioisotope. The polynucleotides are identified in human prostatic			
XX	CC	cancer by differential expression analysis, using DNA microarrays,			
XX	CC	between normal and tumorous tissues, with (over)expression being detected			
XX	CC	by quantitative PCR. Analysis of prostatic cancer samples showed that			
XX	CC	CD24 was upregulated in many of them. Sections of tissue, isolated from			
XX	CC	prostatic cancer patients, or subjects at risk, were incubated			
XX	CC	sequentially with anti-human CD4 murine monoclonal antibodies;			
XX	CC	biotinylated second antibody; streptavidin-conjugated horseradish			
XX	CC	peroxidase and then diaminobenzidine as colour former (brown). The			
XX	CC	samples were counterstained with hemalum (blue). Malignant cells stained			
XX	CC	strongly but non-malignant cells only weakly. In 15 of 63 samples of			
XX	CC	adenocarcinoma, membrane and cytoplasmic staining was very strong, and			
XX	CC	lymph node metastases were also stained. ADR65805-ADR66954 represent the			
XX	CC	polynucleotide and polypeptide sequences used in the method of the			
XX	CC	invention.			
XX	XX	Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;			



Qy 1021 TACTTCCTCCAGCTTTTAAACATTAGATCCCTTCTAGTATCATTCATCCATATCTATATCGGTG 1080  
Db TACTTCCTCCAGCTTTTAAACATTAGATCCCTTCTAGTATCATTCATCCATATCTATATCGGTG 1132  
Qy 1081 CTCCTCAACAGCTCGGAAACACGCTGTGATCCAGGATTTCCACTGATTTATGAATTA 1140  
Db TCTCCAAACAGCTCGGAAACACGCTGTGATCCAGGATTTCCACTGATTTATGAATTA 1192  
Qy 1141 TTTTTCGGGAAACACATTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATCTTA 1200  
Db TTTTTCGGGAAACACATTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATCTTA 1252  
Qy 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACCATGG 1260  
Db CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACCATGG 1312  
Qy 1261 ATGAAAGCTGAAATAAAGCAGTGTGTTTATGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
Db ATGAAAGCTGAAATAAAGCAGTGTGTTTATGACGCTGTATGTGAGAAAAACAAACCCAG 1372  
Qy 1321 GAAATACCTCTTAA 1334  
Db GAAATACCTCTTAA 1386

RESULT 11

ADR66152  
ID ADR66152 standard; DNA; 2755 BP.  
AC ADR66152;  
XX  
XX 02-DEC-2004 (first entry)  
XX Human prostatic carcinoma derived DNA SEQ ID 6 #2.

XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis; ds.  
XX  
XX Homo sapiens.

XX WO2004076614-A2.  
XX  
XX 10-SEP-2004.  
XX  
XX 22-FEB-2004; 2004WO-DE000433.  
XX  
XX 27-FEB-2003; 2003DE-01009985.  
PR 14-MAY-2003; 2003DE-01022134.  
XX

XX (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
XX

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinneemann H, Roepcke S;  
PI Xinzhong L, Staub E;  
XX WPI; 2004-653386/63.  
XX  
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX  
XX Claim 1; Page 481; 1607pp; German.

XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are

CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.  
XX  
SQ Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 13; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGACGGGATCTGCGCGGCTCCAGATGATGTCCTCTCTGGGCGGACGACCCCTAG 60  
Db TTTTCTGGGATCTGCGCGGCTCCAGATGATGTCCTCTCTGGGCGGACGACCCCTAG 112  
Qy 61 TGCTCGTCGCGGTCGCGGCTCCAGATGATGTCCTCTCTGGGCGGACGACCCCTAG 120  
Db TGTCTCGTCGCGGTCGCGGCTCCAGATGATGTCCTCTCTGGGCGGACGACCCCTAG 172  
Qy 121 CTCCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTCTGAGGTGGACAGGA 180  
Db CTCCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTCTGAGGTGGACAGGA 232  
Qy 181 GCGATGAGTCTGTCGGGAAATGTGACTTTTTCATTCGATATCAAAAACCTGGGATGGATA 240  
Db GCGATGAGTCTGTCGGGAAATGTGACTTTTTCATTCGATATCAAAAACCTGGGATGGATA 292  
Qy 241 ATTGGATAAAATTTGTCGGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTCAC 300  
Db ATTGGATAAAATTTGTCGGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTCAC 352  
Qy 301 TCAAGCTGATGTTTATGAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360  
Db TCAAGCTGATGTTTATGAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 412  
Qy 361 CTTTCATGTTATGAGGTTGACTCATTTACACCATTTTCGCAAGCTCAGATTTGGTCTCCAG 420  
Db CTTTCATGTTATGAGGTTGACTCATTTACACCATTTTCGCAAGCTCAGATTTGGTCTCCAG 472  
Qy 421 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 480  
Db AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 532  
Qy 481 ATAGTGTATGTCGGCTTTGGATGGTTTAAGCTTTTACATATAGTCTTACTTCGGAATA 540  
Db ATAGTGTATGTCGGCTTTGGATGGTTTAAGCTTTTACATATAGTCTTACTTCGGAATA 592  
Qy 541 ACTCTTCAGGTGAGAAAGAAAGGATTTGAAAATATTTTATCCAGACATAAAATTTATAAAC 600  
Db ACTCTTCAGGTGAGAAAGAAAGGATTTGAAAATATTTTATCCAGACATAAAATTTATAAAC 652  
Qy 601 TCTCACAGAGACTACTTATTTGCTAAAAGTTAAAGCAGCAGCTACTTACGTCATGGAAAA 660  
Db TCTCACAGAGACTACTTATTTGCTAAAAGTTAAAGCAGCAGCTACTTACGTCATGGAAAA





Db 593 ACTCTTCAGGTGTAGAGAAAGGATTGAAAATATTTATTCAGACATAAAAATTTATAAAC 652  
Qy 601 TCTCACCAGAGACTACTTATTTGCTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAAA 660  
Db 653 TCTCACCAGAGACTACTTATTTGCTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAAA 712  
Qy 661 TTGGTGTCTATAGTCCAGTACATTTGTATAAAGCACCAGCTTTGAAAATGAATCCTCCAC 720  
Db 713 TTGGTGTCTATAGTCCAGTACATTTGTATAAAGCACCAGCTTTGAAAATGAATCCTCCAC 772  
Qy 721 CAGAAAATATAGAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780  
Db 773 CAGAAAATATAGAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 832  
Qy 781 ATGCACACATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAGAGGAATCCTGGAA 840  
Db 833 ATGCACACATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAGAGGAATCCTGGAA 892  
Qy 841 ACCATTTGTATAATGAAAACAAATACCTGACTGTGAAAATGTCAAACTACCCAGTGTG 900  
Db 893 ACCATTTGTATAATGAAAACAAATACCTGACTGTGAAAATGTCAAACTACCCAGTGTG 952  
Qy 901 TCTTCTCCTCAAAAGCTTTTCAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960  
Db 953 TCTTCTCCTCAAAAGCTTTTCAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 1012  
Qy 961 GAAATACACATCTTTTGGTCTGAAGAGATAAGTTTGTATCTGAAATCAAGCTTTCC 1020  
Db 1013 GAAATACACATCTTTTGGTCTGAAGAGATAAGTTTGTATCTGAAATCAAGCTTTCC 1072  
Qy 1021 TACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTCATATCTATATCGGTG 1080  
Db 1073 TACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTCATATCTATATCGGTG 1132  
Qy 1081 CTCAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTATCCA CTGATTTATGAAATTA 1140  
Db 1133 CTCAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTATCCA CTGATTTATGAAATTA 1192  
Qy 1141 TTTTGGGAAACACCTTCAATGCTGAGAGAAAATTTATCGAGAAAACCTGATGTTA 1200  
Db 1193 TTTTGGGAAACACCTTCAATGCTGAGAGAAAATTTATCGAGAAAACCTGATGTTA 1252  
Qy 1201 CAGTTCCTAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACACCATGG 1260  
Db 1253 CAGTTCCTAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACACCATGG 1312  
Qy 1261 ATGAAAAGCTGAATAAAGCAGTGTTTTATGTCACGCTGTATGTGAGAAAACAAAACCCAG 1320  
Db 1313 ATGAAAAGCTGAATAAAGCAGTGTTTTATGTCACGCTGTATGTGAGAAAACAAAACCCAG 1372  
Qy 1321 GAAATACCTCTAAA 1334  
Db 1373 GAAATACCTCTAAA 1386

RESULT 13

ID ADW86762 standard; DNA; 2755 BP.

XX AC ADW86762;

XX AC (first entry)

DT 07-APR-2005 (first entry)

XX Human interferon receptor I encoding DNA.

XX protein interaction; fusion protein; ss; PCR; primer.

XX Homo sapiens.

XX W02005007822-A2.

XX 27-JAN-2005.

XX PF 09-JUL-2004; 2004WO-US021887.  
XX PR 09-JUL-2003; 2003US-0485968P.  
XX PR 15-OCT-2003; 2003US-0511918P.  
XX PR 27-APR-2004; 2004US-0566113P.  
XX PA (SENT-) SENTIGEN BIOSCIENCES INC.  
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX PI Lee KJ, Axel R, Strapps W, Barnea G;  
XX XX WPI; 2005-102091/11.  
XX PT Determining protein/protein interaction modulator comprises contacting  
XX PT the compound to a cell transfected or transfected with G-protein coupled  
XX PT receptor and arrestin.  
XX PS Example 24; SEQ ID NO 81; 133pp; English.  
XX CC The invention relates to a novel method for determining if a test-  
XX CC compound modulates a specific protein/protein interaction or protein  
XX CC interactions of interest. The method comprises contacting the compound to  
XX CC a cell or samples of cells, each of which has been transfected or  
XX CC transfected with a nucleic acid molecule. The invention further  
XX CC comprises: a recombinant cell, transfected or transfected with any of the  
XX CC nucleic acid molecules; an isolated nucleic acid molecule comprising, in  
XX CC 5' to 3' order, any of the nucleotide sequences described; an expression  
XX CC vector comprising the isolated nucleic acid molecule of above, operably  
XX CC linked to a promoter; a fusion protein produced by expression of the  
XX CC isolated nucleic acid molecule of above; and a test kit, useful for  
XX CC determining if a test compound modulates a specific protein/protein  
XX CC interaction of interest. The methods, nucleic acid molecules, and kit are  
XX CC useful for determining if a test-compound modulates a specific  
XX CC protein/protein interaction or protein interactions of interest. This  
XX CC polynucleotide sequence represents the human interferon receptor I  
XX CC encoding DNA used in the method of the invention.  
XX SQ Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 14; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGACGGGATCTCGGGGGCTCCAGATGATGGTCTCTCTGGGGCGACACCCCTAG 60  
Db 53 CTGGTGGGATCTCGGGGGCTCCAGATGATGGTCTCTCTGGGGCGACACCCCTAG 112  
Qy 61 TGTCTCTCGCGCTGGGGCCCATGGTCTTGTCCGACGCGCAGGTGGAAAAAATCTAAAT 120  
Db 113 TGTCTCTCGCGCTGGGGCCCATGGTCTTGTCCGACGCGCAGGTGGAAAAAATCTAAAT 172  
Qy 121 CTCCTCAAAAAGTGAAGTTCGACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 180  
Db 173 CTCCTCAAAAAGTGAAGTTCGACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 232  
Qy 181 GCGATGAGTCTGTCCGGGAATGTGACATTTTTCATTCGATTTATCAAAAACCTGGGATGATA 240  
Db 233 GCGATGAGTCTGTCCGGGAATGTGACATTTTTCATTCGATTTATCAAAAACCTGGGATGATA 292  
Qy 241 ATTGGATAAAAATGTCTGGGTGTGAGAAATTTACTAGTACCAATGCAACTTTTCTTCAC 300  
Db 293 ATTGGATAAAAATGTCTGGGTGTGAGAAATTTACTAGTACCAATGCAACTTTTCTTCAC 352  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTTAAATTTGGGTATAGAGCAGAAAAAACAACCTT 360  
Db 353 TCAAGCTGAATGTTTATGAAGAAATTTAAATTTGGGTATAGAGCAGAAAAAACAACCTT 412  
Qy 361 CTTTCATGTTATGAGTGTGACTCATTTTACACCATTTTCGCAAGCTCAGATTTGGTCTCCAG 420  
Db 413 CTTTCATGTTATGAGTGTGACTCATTTTACACCATTTTCGCAAGCTCAGATTTGGTCTCCAG 472  
Qy 421 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCTGGAACAAAAG 480

Db 473 AAGTACATTTAGAGCTGAGATAGGCATAGTGATACATCTCTCTCGAACAAAG 532  
Qy 481 ATAGTGTTATGCGGCTTTGGATGGTTAAAGCTTTTACATATAGCTTACTTATCTGGA 540  
Db 533 ATAGTGTTATGCGGCTTTGGATGGTTAAAGCTTTTACATATAGCTTACTTATCTGGA 592  
Qy 541 ACTCTTCAGGTGTAGAGAAAGGATTGAANAATATTATTCCAGACATATAAATTTTATAAC 600  
Db 593 ACTCTTCAGGTGTAGAGAAAGGATTGAANAATATTATTCCAGACATATAAATTTTATAAC 652  
Qy 601 TCTCACCAGAGACTACTTATTGTCTAAAGTTAAAGCAGCAGCTACTTACGTCTGCGA 660  
Db 653 TCTCACCAGAGACTACTTATTGTCTAAAGTTAAAGCAGCAGCTACTTACGTCTGCGA 712  
Qy 661 TTGGTGCTATAGTCCAGTACATTTGTATTAAGACACAGTTTGAANAATGAATCTCCTCAC 720  
Db 713 TTGGTGCTATAGTCCAGTACATTTGTATTAAGACACAGTTTGAANAATGAATCTCCTCAC 772  
Qy 721 CAGAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
Db 773 CAGAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 832  
Qy 781 ATGCAAAACATGACCTTTTCAAGTTCAAGTGTCCAGCTTCTCCGCGTAAAGGAATCTCGAA 840  
Db 833 ATGCAAAACATGACCTTTTCAAGTTCAAGTGTCCAGCTTCTCCGCGTAAAGGAATCTCGAA 892  
Qy 841 ACCATTTGTATAAATGGAAACAAATACCTGCTGTGAAATGTCAAAATCTACCCAGTGTG 900  
Db 893 ACCATTTGTATAAATGGAAACAAATACCTGCTGTGAAATGTCAAAATCTACCCAGTGTG 952  
Qy 901 TCTTCTCTCAAAACGTTTTTCAAAAGGAATTTACCTTCTCCGCGTCAAGCATCTGATG 960  
Db 953 TCTTCTCTCAAAACGTTTTTCAAAAGGAATTTACCTTCTCCGCGTCAAGCATCTGATG 1012  
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC 1020  
Db 1013 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC 1072  
Qy 1021 TACTTCTCTCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTG 1080  
Db 1073 TACTTCTCTCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTG 1132  
Qy 1081 CTCGAAACAGTCTGGAACACGCGCTGTGATCCAGGATTCCTAGTATTTATGAATTA 1140  
Db 1133 CTCGAAACAGTCTGGAACACGCGCTGTGATCCAGGATTCCTAGTATTTATGAATTA 1192  
Qy 1141 TTTTGTGGGAAACACATTCGAATCTGAGAGAAATTTATCGAGAAATTAATCTGATGTTA 1200  
Db 1193 TTTTGTGGGAAACACATTCGAATCTGAGAGAAATTTATCGAGAAATTAATCTGATGTTA 1252  
Qy 1201 CAGTTCTCTAAATTTGAAACCACTGCTGTATATTGTGTGAAGCCAGACACACCATGG 1260  
Db 1253 CAGTTCTCTAAATTTGAAACCACTGCTGTATATTGTGTGAAGCCAGACACACCATGG 1312  
Qy 1261 ATGAAAGCTCAATATAAAGCAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAACAAACAG 1320  
Db 1313 ATGAAAGCTCAATATAAAGCAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAACAAACAG 1372  
Qy 1321 GAAATACCTCTAAA 1334  
Db 1373 GAAATACCTCTAAA 1386

RESULT 14

AAQ11701

ID AAQ11701 standard; DNA; 2784 BP.

XX AC

AAQ11701;

XX AC

DT 18-JUL-1991 (first entry)

XX DT

DE Human alpha-interferon receptor protein encoding sequence.

XX KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent; drug targeting; ss.  
XX OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 79..1752  
FT FT /\*tag= a  
FT FT /product= "human alpha IFN"  
FT FT sig\_peptide 79..159  
FT FT /\*tag= b  
FT FT /product= "signal peptide"  
FT FT misc\_RNA 226..234  
FT FT /\*tag= c  
FT FT misc\_RNA 250..258  
FT FT /label= glycosylation site  
FT FT /\*tag= d  
FT FT /label= glycosylation site  
FT FT misc\_RNA 319..327  
FT FT /\*tag= e  
FT FT /label= glycosylation site  
FT FT misc\_RNA 340..348  
FT FT /\*tag= f  
FT FT /label= glycosylation site  
FT FT misc\_RNA 406..414  
FT FT /\*tag= g  
FT FT /label= glycosylation site  
FT FT misc\_RNA 592..600  
FT FT /\*tag= h  
FT FT /label= glycosylation site  
FT FT misc\_RNA 838..847  
FT FT /\*tag= i  
FT FT /label= glycosylation site  
FT FT misc\_RNA 1015..1023  
FT FT /\*tag= j  
FT FT /label= glycosylation site  
FT FT misc\_RNA 1018..1026  
FT FT /\*tag= k  
FT FT /label= glycosylation site  
FT FT misc\_RNA 1204..1212  
FT FT /\*tag= l  
FT FT /label= glycosylation site  
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FT FT misc\_RNA 1375..1383  
FT FT /\*tag= n  
FT FT /label= glycosylation site  
FT FT misc\_RNA 1597..1605  
FT FT /\*tag= o  
FT FT /label= glycosylation site  
FT FT misc\_RNA 1630..1638  
FT FT /\*tag= p  
FT FT /label= glycosylation site  
FT FT misc\_RNA 1687..1695  
FT FT /\*tag= q  
FT FT /label= glycosylation site  
XX WO9105862-A.  
XX 02-MAY-1991.  
XX PF 20-OCT-1989; 89FR-00013770.  
XX PR 20-OCT-1989; 89FR-00013770.  
XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX PI Mogensen K, Lutfalla G, Gresser I;  
XX WPI; 1991-148740/20.  
XX P-PSDB; AAR11958.  
DR DR

XX New human alpha-interferon receptor protein - useful for testing  
PT interferon agonists and in treatment or diagnosis.  
XX

PS Disclosure; Fig 4; 30pp; French.

XX This sequence encodes a recombinant human alpha interferon (IFN) receptor  
CC protein useful for the testing of IFN agonists and for treatment and  
CC diagnosis of viral diseases and tumours. Antibodies raised against this  
CC protein can be used for blocking the receptor when required, e.g. where  
CC overexpression of alpha-IFN is harmful. The Abs are also useful for e.g.  
CC drug targeting. Variants of the protein, having residue 184 (Ihr)  
CC replaced by Arg and an Asp in- serted between residues 479 and 480, are  
XX also useful

SQ Sequence 2784 BP; 896 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 2; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGGAGTCTGGCGGCTCCAGATGATGTCCTCTCGGGCGCGACGCCCTAG 60  
DB 53 CTGTGGGATCTGGCGGCTCCAGATGATGTCCTCTCGGGCGCGACGCCCTAG 112  
QY 61 TGCTCGTCGCGCGTGGGCCCATGGGTGTTGCCGAGCGCGAGGTGGAAAAATCTAAAT 120  
DB 113 TGCTCGTCGCGTGGGCCCATGGGTGTTGCCGAGCGCGAGGTGGAAAAATCTAAAT 172  
QY 121 CTCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCAGAGTGGAAACAGGA 180  
DB 173 CTCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCAGAGTGGAAACAGGA 232  
QY 181 GCGATGAGTCTGCGGGAATGTGACTTTTCATTCGATATCAAAAACCTGGGATGGATA 240  
DB 233 GCGATGAGTCTGCGGGAATGTGACTTTTCATTCGATATCAAAAACCTGGGATGGATA 292  
QY 241 ATTGGATAAAATTTCTCGGGTGTGAGATATTTACTAGTACCAATGCAACTTTTCTTCAC 300  
DB 293 ATTGGATAAAATTTCTCGGGTGTGAGATATTTACTAGTACCAATGCAACTTTTCTTCAC 352  
QY 301 TCAAGCTGAATGTTTATGAGAAATTAATTTGCGTATAAGAGCGAGAAAGAAACACTT 360  
DB 353 TCAAGCTGAATGTTTATGAGAAATTAATTTGCGTATAAGAGCGAGAAAGAAACACTT 412  
QY 361 CTTTCATGATGAGTGTGACTCAATTTACACATTTCCGAAAGCTCAGATTGCTCCACG 420  
DB 413 CTTTCATGATGAGTGTGACTCAATTTACACATTTCCGAAAGCTCAGATTGCTCCACG 472  
QY 421 AAGTACATTTAGAGCTGAAGATAAGCAATGATGATACACATCTCTCTGGAAACAAAG 480  
DB 473 AAGTACATTTAGAGCTGAAGATAAGCAATGATGATACACATCTCTCTGGAAACAAAG 532  
QY 481 ATAGTGTATGCGGCTTTGATGGTTTAAAGTTTAACTTATAGCTTACTTATCTGGAAAA 540  
DB 533 ATAGTGTATGCGGCTTTGATGGTTTAAAGTTTAACTTATAGCTTACTTATCTGGAAAA 592  
QY 541 ACTCTTCAGGTGTAGAGAAAGGATTCGAAATATTTATTCAGACATAAATTTATTAAC 600  
DB 593 ACTCTTCAGGTGTAGAGAAAGGATTCGAAATATTTATTCAGACATAAATTTATTAAC 652  
QY 601 TCTCACCAGAGACTACTTTATTTGCTTAAAGTTTAAAGCAGCACTACTTACGTGCAAGAAA 660  
DB 653 TCTCACCAGAGACTACTTTATTTGCTTAAAGTTTAAAGCAGCACTACTTACGTGCAAGAAA 712  
QY 661 TTGCTGTCTATPAGTCCAGTACATTTGTATAAGACCAAGTTGAAATGAACCTCCAC 720  
DB 713 TTGCTGTCTATPAGTCCAGTACATTTGTATAAGACCAAGTTGAAATGAACCTCCAC 772  
QY 721 CAGAAATATAGAGTCAAGTGTCCAAATCAGACTATGTTCTTAAATGGATATACAT 780  
DB 773 CAGAAATATAGAGTCAAGTGTCCAAATCAGACTATGTTCTTAAATGGATATACAT 832

QY 781 ATCAAAACATGACCTTTCAAGTTCAAGTTCAGTGGCTCCACGCTTTTAAAGAAATCCTCGAA 840  
DB 833 ATCAAAACATGACCTTTCAAGTTCAAGTTCAGTGGCTCCACGCTTTTAAAGAAATCCTCGAA 892  
QY 841 ACCATTTGTATTAATGGAACCAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900  
DB 893 ACCATTTGTATTAATGGAACCAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 952  
QY 901 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCTACCAAGCATCTCATG 960  
DB 953 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCTACCAAGCATCTCATG 1012  
QY 961 GAAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAATCAAGCTTTCC 1020  
DB 1013 GAAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAATCAAGCTTTCC 1072  
QY 1021 TACTTCTCCAGTCTTTAACTTAGATCCCTTAGTGTATTCATTTCCATATCTATATCCGTG 1080  
DB 1073 TACTTCTCCAGTCTTTAACTTAGATCCCTTAGTGTATTCATTTCCATATCTATATCCGTG 1132  
QY 1081 CTCAAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1140  
DB 1133 CTCAAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1192  
QY 1141 TTTTGGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
DB 1193 TTTTGGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252  
QY 1201 CAGTTCTTAATTTGAAACCACTGATATATTTGTGTAAGCCAGAGCAACACCATGG 1260  
DB 1253 CAGTTCTTAATTTGAAACCACTGATATATTTGTGTAAGCCAGAGCAACACCATGG 1312  
QY 1261 ATCAAAAGCTGAATAAAAGCAGTGTGTTTAGTCAGCTGTATGTGAGAAAAACAAACAG 1320  
DB 1313 ATCAAAAGCTGAATAAAAGCAGTGTGTTTAGTCAGCTGTATGTGAGAAAAACAAACAG 1372  
QY 1321 GAAATACCTCTAAA 1334  
DB 1373 GAAATACCTCTAAA 1386

RESULT 15  
AAF16297  
ID AAF16297 standard; cDNA; 2017 BP.  
XX  
AC AAF16297;  
XX  
XX 13-MAR-2001 (first entry)  
DT  
XX Human prostate cancer antigen nucleotide sequence SEQ ID NO:732.  
DE  
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytostatic; cardiocactive; immunomodulatory; muscular;  
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200055174-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US005988.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
PI Rosen CA, Ruben SM;  
XX

DR WPI: 2000-587513/55.  
XX P-PSDB; AAB57094.  
PT Prostate cancer associated gene sequences, referred to as prostate cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as prostate cancer.  
XX  
PS Claim 1; Page 1157; 2338pp; English.  
XX  
CC AAF15566 to AAF16505 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytostatic,  
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotropic, antiinfective, gynecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
CC AAB57303 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 2017 BP; 665 A; 377 C; 413 G; 559 T; 0 U; 3 Other;  
Query Match 98.8%; Score 1327.2; DB 3; Length 2017;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1329; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CTGCAGGATCTGCGGCGCTCCAGATGATGCTGCTCTCGGCGCGAGCCCTAG 60  
DB |||||  
QY 59 CTGTGGATCTGCGGCGCTCCAGATGATGCTGCTCTCGGCGCGAGCCCTAG 118  
DB |||||  
QY 61 TGCTCGTCCGCTGGCGCCATGGGTGTTGTCGCGAGCGCGAGGTGGAATAATCTAAAT 120  
DB |||||  
QY 119 TGCTCGTCCGCTGGCGCCATGGGTGTTGTCGCGAGCGCGAGGTGGAATAATCTAAAT 178  
DB |||||  
QY 121 CTCCTCAAAAGTAGAGTGCACATCATAGATGACATTTTATCTGAGGTGGACAGGA 180  
DB |||||  
QY 179 CTCCTCAAAAGTAGAGTGCACATCATAGATGACATTTTATCTGAGGTGGACAGGA 238  
DB |||||  
QY 181 GCGATGATCTGTCGGGATGACTTTTTCATTCGATATCAAAAATCTGGATGGATA 240  
DB |||||  
QY 239 GCGATGATCTGTCGGGATGACTTTTTCATTCGATATCAAAAATCTGGATGGATA 298  
DB |||||  
QY 241 ATTGATAAATTTGTCGGGTGTCAGATATTTACTAGTACCAATTTCTTCTCAC 300  
DB |||||  
QY 299 ATTGATAAATTTGTCGGGTGTCAGATATTTACTAGTACCAATTTCTTCTCAC 358  
DB |||||  
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGGTATAGAGCAGAAAGAACACTT 360  
DB |||||  
QY 359 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGGTATAGAGCAGAAAGAACACTT 418  
DB |||||  
QY 361 CTTGATGATGAGGTGACTCAATTTACCAATTTGCGAAAGCTCAGATTGGTCTCCAG 420  
DB |||||  
QY 419 CTTGATGATGAGGTGACTCAATTTACCAATTTGCGAAAGCTCAGATTGGTCTCCAG 478  
DB |||||  
QY 421 AAGTACATTTAGAGCTCAAGATAGGCAATAGTATGATACATCTCTCTGGAACAAAG 480  
DB |||||  
QY 479 AAGTACATTTAGAGCTCAAGATAGGCAATAGTATGATACATCTCTCTGGAACAAAG 538  
DB |||||  
QY 481 ATAGTGTATGTTGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTTACTTATCTGGA 540  
DB |||||  
QY 539 ATAGTGTATGTTGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTTASTTATCTG 598  
DB |||||  
QY 541 ACTCTTCAGGTGTAGAAGAAAGATTGAAATATATTTATTCAGACATATAATTTATAAC 600  
DB |||||  
QY 599 ACTCTTCAGGTGTAGAAGAAAGATTGAAATATATTTATTCAGACATATAATTTATAAC 658  
DB |||||  
QY 601 TCTCACCAGAGACTACTTTATTTGCTTAAAGTTAAAGCAGCACTTACGTCATGGGAA 660  
DB |||||  
QY 659 TCTCACCAGAGACTACTTTATTTGCTTAAAGTTAAAGCAGCACTTACGTCATGGGAA 718  
DB |||||

Search completed: January 17, 2006, 19:48:55  
Job time : 877 secs

QY 661 TTGCTGTCTATAGTCCAGTACATTTGTATAAAGCAGCCAGTTGAAATGAACTACTCTCCAC 720  
DB |||||  
QY 719 TTGCTGTCTATAGTCCAGTACATTTGTATAAAGCAGCCAGTTGAAATGAACTACTCTCCAC 778  
DB |||||  
QY 721 CAGAAATATAGAAGTCAAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780  
DB |||||  
QY 779 CAGAAATATAGAAGTCAAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTATACAT 838  
DB |||||  
QY 781 ATGCAAAATGACCTTTTCAAGTTCAGTGGTCCAGCGCTTTTAAAAAGGAATCTTGAA 840  
DB |||||  
QY 839 ATGCAAAATGACCTTTTCAAGTTCAGTGGTCCAGCGCTTTTAAAAAGGAATCTTGAA 898  
DB |||||  
QY 841 ACCATTTGTATAAATGGAAACAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900  
DB |||||  
QY 899 ACCATTTGTATAAATGGAAACAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 958  
DB |||||  
QY 901 TCTTTCTCAAAAGCTTTTCAAAAGGAATTTACCTTCTCGCGTCAAGCATCTGTATG 960  
DB |||||  
QY 959 TCTTTCTCAAAAGCTTTTCAAAAGGAATTTACCTTCTCGCGTCAAGCATCTGTATG 1018  
DB |||||  
QY 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATACCTGAATAACAAGCTTTCC 1020  
DB |||||  
QY 1019 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATACCTGAATAACAAGCTTTCC 1078  
DB |||||  
QY 1021 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTATTCTATCCATATCTATATCGTG 1080  
DB |||||  
QY 1079 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTATTCTATCCATATCTATATCGTG 1138  
DB |||||  
QY 1081 CTCCAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTATCCACTGATTTTATGAAATTA 1140  
DB |||||  
QY 1139 CTCCAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTATCCACTGATTTTATGAAATTA 1198  
DB |||||  
QY 1141 TTTTTCGGGAAAACACTTCAAAATGCTGAGAGAAAATTTATCGAGAAAATTAATCTGATGTTA 1200  
DB |||||  
QY 1199 TTTTTCGGGAAAACACTTCAAAATGCTGAGAGAAAATTTATCGAGAAAATTAATCTGATGTTA 1258  
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QY 1201 CAGTTCCTAATTTGAAACCACTGATGATATTGTTGTAAGCCAGAGCAGACACACCATGG 1260  
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QY 1259 CAGTTCCTAATTTGAAACCACTGATGATATTGTTGTAAGCCAGAGCAGACACACCATGG 1318  
DB |||||  
QY 1261 ATGAAAAGCTGAATAAAGCAGCTGTTTATGTCAGCTGTATGTGAGAAAACAAAACCCAG 1320  
DB |||||  
QY 1319 ATGAAAAGCTGAATAAAGCAGCTGTTTATGTCAGCTGTATGTGAGAAAACAAAACCCAG 1378  
DB |||||  
QY 1321 GAAATACCTCTAAA 1334  
DB |||||  
QY 1379 GAAATACCTCTAAA 1392  
DB |||||

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 19:30:55 ; Search time 5826 Seconds  
(without alignments)  
10785.282 Million cell updates/sec

Title: US-10-824-981-1  
Perfect score: 1343  
Sequence: 1 ctgcaggatctgcggcgc.....ataccttaaatgaggtacc 1343

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hc.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gss1.\*  
10: gb\_gss2.\*  
11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943.6	70.3	1042	5	BX417950
2	840.8	62.6	1073	3	BM476333 AGENCOURT
3	800.8	59.6	1440	11	DQ035425 Homo sapi
4	756.2	56.3	876	5	BQ440937 AGENCOURT
5	750.8	55.9	807	1	AU133717
6	721.8	53.7	820	2	BG613775
7	716.8	53.4	918	3	BM457086 AGENCOURT
8	713.2	53.1	1042	2	BE739817
9	692	51.5	880	1	AU136208
10	680.2	50.6	938	3	BM465808 AGENCOURT
11	673.6	50.2	784	2	BG618347
12	662.4	49.3	843	6	CD109826 AGENCOURT
13	649.4	48.4	674	5	BX356887
14	633	47.1	699	1	ALU707406
15	632	47.1	678	6	CD697468
16	631	47.0	920	3	BM452951
17	629.6	46.9	1154	2	BF341745
18	629	46.8	651	7	CN425394
19	618.8	46.1	643	7	CV029361
20	618.6	46.1	868	2	BG506738
21	606.6	45.2	787	3	BI552718
22	602.6	44.9	810	3	BI463822

23	598.6	44.6	772	3	BI828029
24	589.6	43.9	933	2	BF037597
25	571.6	42.6	619	2	BE315416
26	567	42.2	581	3	BP288799
27	557.4	41.5	570	3	BP207712
28	556.4	41.4	645	2	BE467210
29	553.6	41.2	643	1	AL708297
30	549.4	40.9	581	3	BP311974
31	548	40.8	677	2	BG698419
32	546.4	40.7	613	3	BP237485
33	543	40.4	590	7	CN425393
34	542.8	40.4	873	2	BE780158
35	542	40.4	615	2	BG819073
36	541	40.3	582	3	BP302170
37	533.6	39.7	686	2	BG548299
38	530.4	39.5	599	1	AW960402
39	528.6	39.4	639	7	CR856996
40	527.4	39.3	594	3	BP238840
41	527	39.2	582	3	BP332742
42	525.6	39.1	588	8	DN994934
43	524	39.0	627	1	AU137565
44	523	38.9	823	3	BP157720
45	520.8	38.8	584	3	BP242448

#### ALIGNMENTS

RESULT 1  
BX417950  
LOCUS BX417950 1042 bp mRNA linear EST 03-MAY-2004  
DEFINITION BX417950 Homo sapiens PLACENTA Homo sapiens CDNA clone CS0DE014YB03  
5-PRIME, mRNA sequence.  
ACCESSION BX417950  
VERSION BX417950.2 GI:46955956  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1042)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length CDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 15, 2003 this sequence version replaced gi:30767795.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 10373.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0DE014CA02QPI&c=10373.f.  
Location/Qualifiers  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

ORIGIN



Query Match		70.3%; Score 943.6; DB 5; Length 1042;
Best Local Similarity		97.4%; Pred. No. 5.9e-226;
Matches		968; Conservative 10; Mismatches 14; Indels 2; Gaps 2;
QY	1	CTCGAGGGATCTCGGGCGGCTCCAGATGATGTCGTCTCTCGGGCGGACGACCCCTAG 60
DB	47	CTGGTGGGATCTCGGGCGGCTCCAGATGATGTCGTCTCTCGGGCGGACGACCCCTAG 106
QY	61	TGCTCTGTCGCGCGGCGCCATGGTGTGTCGCGAGCGGAGGTGGAAAAATCTAAAT 120
DB	107	TGCTCTGTCGCGCGGCGCCATGGTGTGTCGCGAGCGGAGGTGGAAAAATCTAAAT 166
QY	121	CTCCTCAAAAAGTAGAGGTGCACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 180
DB	167	CTCCTCAAAAAGTAGAGGTGCACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 226
QY	181	GCATGAGTCTGTCGGGAATGTCATTTTTCATTCGATATCAAAAACCTGGGATGGATA 240
DB	227	GCATGAGTCTGTCGGGAATGTCATTTTTCATTCGATATCAAAAACCTGGGATGGATA 286
QY	241	ATTGGATAAAATGTCGCGGTGCAGAAATTAATAGTACCAATGCAACTTTTCTTCAC 300
DB	287	ATTGGATAAAATGTCGCGGTGCAGAAATTAATAGTACCAATGCAACTTTTCTTCAC 346
QY	301	TCAAGCTGAATGTTATGAAAGAAATTAATTTGGGTATAGAGCAGAGAAAAACACATT 360
DB	347	TCAAGCTGAATGTTATGAAAGAAATTAATTTGGGTATAGAGCAGAGAAAAACACATT 406
QY	361	CTTCATGTTAGAGTTGACTCAATTTTACACCAATTCGAAAGCTCAGATGGTCTCCAG 420
DB	407	CTTCATGTTAGAGTTGACTCAATTTTACACCAATTCGAAAGCTCAGATGGTCTCCAG 466
QY	421	AAGTACATTTAGAGCTGAAGTAAGCAATAGTATACATCTCTCTGGAAACAAAG 480
DB	467	AAGTACATTTAGAGCTGAAGTAAGCAATAGTATACATCTCTCTGGAAACAAAG 526
QY	481	ATAGTGTATGTCGGGCTTTCCGATGGTTTAACTTTACATATAGCTTACTTATCTGAAAA 540
DB	527	ATAGTGTATGTCGGGCTTTCCGATGGTTTAACTTTACATATAGCTTACTTATCTGAAAA 586
QY	541	ACTCTTCAGGTGAGAAAGAGATTGAAATATTTTATTCAGACATATAAATTTATAAAC 600
DB	587	ACTCTTCAGGTGAGAAAGAGATTGAAATATTTTATTCAGACATATAAATTTATAAAC 646
QY	601	TCTCACCAGACTACTTATTTGCTAAAAGTTAAGCAGCACTTACTGCTCATGGAAA 660
DB	647	TCTCACCAGACTACTTATTTGCTAAAAGTTAAGCAGCACTTACTGCTCATGGAAA 706
QY	661	TTGGTGTCTATAGTCCAGTACATTTGTATAAGACCACAGTTGAAAAATGAACCTCCAC 720
DB	707	TTGGTGTCTATAGTCCAGTACATTTGTATAAGACCACAGTTGAAAAATGAACCTCCAC 766
QY	721	CAGAAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTACAT 780
DB	767	CAGAAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTACAT 826
QY	781	ATCBAACATGACCTTTCAGTTTCAGTGTCCACGCTTTTAAAGAGAAATCTCTGGAA 840
DB	827	ATCBAACATGACCTTTCAGTTTCAGTGTCCACGCTTTTAAAGAGAAATCTCTGGAA 886
QY	841	ACCAATTTGATAAATGAAAAACAAATACCTGCTGT - GAAAAATGTCAAAATCTACCAAGTGT 899
DB	887	ACCAATTTGATAAATGAAAAACAAATACCTGCTGTGGAANAATGTCAAACTACCAAGTGT 946
QY	900	GTCTTTCTCAAAACGTTTTTCCAAAAGAAATTTACTCTCCGCGTACAAAGCATCTGAT 959
DB	947	GTCTTTCTCAAAACGTTTTTCCAAAAGG - AWTATCCTTCYCCGCGTACAAACATCTGAT 1005
QY	960	GGAAATAACACATCTTTTGGTCTGAGAGATAA 993
DB	1006	GGAAATAACACATCTTTTGGTCTGAGRRRAAAA 1039
RESULT 2		
BM476333		
LOCUS		
DEFINITION		BM476333 1073 bp mRNA linear EST 05-FEB-2002
ACCESSION		AGENCOURT_6479121 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:558971
VERSION		5', mRNA sequence.
KEYWORDS		BM476333.1 GI:18525375
SOURCE		EST.
ORGANISM		Homo sapiens (human)
REFERENCE		Homo sapiens
AUTHORS		Homo sapiens
TITLE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
JOURNAL		1 (bases 1 to 1073)
COMMENT		NIH-MGC http://mgi.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1282 row: m column: 20 High quality sequence stop: 736.
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		/db_xref="taxon:9606"
		/clone="IMAGE:558971"
		/cissue_type="duodenal adenocarcinoma, cell line"
		/lab_host="DH10B (phage-resistant)"
		/clone_lib="NIH MGC 88"
		/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN		
Query Match		62.5%; Score 840.8; DB 3; Length 1073;
Best Local Similarity		94.1%; Pred. No. 4.1e-200;
Matches		928; Conservative 0; Mismatches 49; Indels 9; Gaps 5;
QY	1	CTGCAGGGATCTCGCGCGGCTCCAGATGATGTCGTCTCTCGGGCGGACGACCCCTAG 60
DB	66	CTGGTGGGATCTGCGCGGCTCCAGATGATGTCGTCTCTCGGGCGGACGACCCCTAG 125
QY	61	TGCTCTGTCGCGGTGGGCCCATGGGTGTCGCGAGCGGAGGTGGAAAAATCTAAAT 120
DB	126	TGCTCTGTCGCGGTGGGCCCATGGGTGTCGCGAGCGGAGGTGGAAAAATCTAAAT 185
QY	121	CTCCTCAAAAAGTAGAGGTGCACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 180
DB	186	CTCCTCAAAAAGTAGAGGTGCACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 245
QY	181	GCATGAGTCTGTCGGGAATGTGACCTTTTTCATTTCGATTATCAAAAACTGGGATGGATA 240
DB	246	GCATGAGTCTGTCGGGAATGTGACCTTTTTCATTTCGATTATCAAAAACTGGGATGGATA 305
QY	241	ATTGGATAAAATGTCGCGGTGCAGAAATTAATAGTACCAATGCAACTTTTCTTCAC 300
DB	306	ATTGGATAAAATGTCGCGGTGCAGAAATTAATAGTACCAATGCAACTTTTCTTCAC 365
QY	301	TCAAGCTGAATGTTTATGAAAGAAATTAATTTGGTATAGAGCAGAGAAAAACACATT 360
DB	366	TCAAGCTGAATGTTTATGAAAGAAATTAATTTGGTATAGAGCAGAGAAAAACACATT 425
QY	361	CTTCATGATGAGGTTGACTCATTTTACACCAATTTTCGAAAGCTCAGATTGGTCTCCAG 420

426	Db	CTTCATGGTATGAGTTGACTCACTTTACCAATTTGCGAAAGCTCAGATTGGTCTCTCCAG	485
421	Qy	AAGTACATNTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG	480
486	Db	AAGTACATNTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG	545
481	Qy	ATAGTGTATTGTGGGCTTTCGGATGGTTAAGCTTTACATATAGCTTACTTATCTGGAAAA	540
546	Db	ATAGTGTATTGTGGGCTTTCGGATGGTTAAGCTTTACATATAGCTTACTTATCTGGAAAA	605
541	Qy	ACTCTTCAGCTGTAGAGAAAGGATTGAAAATATTATTTCAGACATAAAATTTATAAAC	600
606	Db	ACTCTTCAGCTGTAGAGAAAGGATTGAAAATATTATTTCAGACATAAAATTTATAAAC	665
601	Qy	TCTCAACAGAGACTACTTATTGTCTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA	660
666	Db	TCTCAACAGAGACTACTTATTGTCTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA	725
661	Qy	TTGGTGTCTATAGTCCAGTACATTGTATATAAGACACAGTGTGAAAAATGAACTACTCTCCAC	720
726	Db	TTGGTGTCTATAGTCCAGTACATTGTATATAAGACACAGTGTGAAAAATGAACTACTCTCCAC	785
721	Qy	CAGAAAATATAGAACTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT	780
786	Db	CAG-AAATATAGAACTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT	844
781	Qy	ATCGAAACATGACCTTTTCAAGTTCAGTGGCTCCAC-GCCTTTTTTAAAAAGGAATCTCTGGA	839
845	Db	ATCGAAACATGACCTTTTCAAGTTCAGTGGCTCCCGGCTTTTTTAAAAAGGNACTCTGGA	904
840	Qy	AACCATTTGTATAAATCGAAACAAATACCTGA--CTGTGAAAATGTCAAAACTTACCAGT	897
905	Db	AACCATTTGTATAAATCGAAACCAATACCTGNACTGGGGGAAAATGTCAAAAACCTACGCCG	964
898	Qy	GTGT--CTTTCCTCAAAAGCTTTTCCAAAAGGAA--TTTACCTCTCTCGCGTCAACAGC	952
965	Db	NTGTGTCTTTCTTCAAAAAGTTTTTTTCCAAAAGNAATTTACCTTTCTTCGGGGAAACAC	1024
953	Qy	ATCTGATGGAAATAACACATCTTTTT	978
1025	Db	ATCTGGATGGGAAAAACCACTCCTT	1050

RESULT 3	
LOCUS	DQ035425
DEFINITION	Homo sapiens IFNARI gene, VIRTUAL TRANSCRIPT, partial sequence, linear GSS 02-JUN-2005
ACCESSION	DQ035425
VERSION	DQ035425.1
KEYWORDS	GSS
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1440)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL	(et) PLOS Biol. 3 (6), E170 (2005)
PUBMED	15869325
REFERENCE	2 (bases 1 to 1440)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering

them based on alignment. Translation starts at the beginning of alignment.

FEATURES	Location/Qualifiers
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gene	
ORIGIN	
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Best Local Similarity	61.3%; Pred. No. 4.9e-190;
Matches 802; Conservative	0; Mismatches 506; Indels 0; Gaps 0;
QY	27 ATGATGGTCTCTCTCGGCGCGACACCTAGTGTCTGTCGCGGTGGGCCCATGGGTG 86
Db	1 ATGATGGTCTCTCTCGGCGCGACACCTAGTGTCTGTCGCGGTGGGCCCATGGGTG 60
QY	87 TTGTCCGACGCCGAGGTGGAAAAATCTAAAAATCTCTCAAAAAGTAGAGGTGCATC 146
Db	61 TTGTCCGACGCCGAGGTGGAAAAATCTAAAAATCTCTCAAAAAGTAGAGGTGCATC 120
QY	147 ATAGATGACAACCTTTATCTGAGGTGGAAACAGCGCATGAGTGTGTCGGGAATGTCAT 206
Db	121 ATAGATGACAACCTTTATCTGAGGTGGAAACAGCGCATGAGTGTGTCGGGAATGTCAT 180
QY	207 TTTTTCATTCGATTATCAAAAAATCGGATGCGATAATTGGATAAAAATGTCTGGGTGTG 266
Db	181 TTTTTCATTCGATTATCAAAAAATCGGATGCGATAATTGGATAAAAATGTCTGGGTGTG 240
QY	267 AATATTACTAGTACCAATCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAATT 326
Db	241 AATATTACTAGTACCAATCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAATT 300
QY	327 AAATTGGGTATAGAGCAGAAAAAGAAAAACACTTCTCATGGTATGAGGTGACTCATTT 386
Db	301 AAATTGGGTATAGAGCAGAAAAAGAAAAACACTTCTCATGGTATGAGGTGACTCATTT 360
QY	387 ACACCATTCGCAAAAGCTCAGATTGGTCTCCAGAAGTACATTTAGAAGCTGAAGATAAG 446
Db	361 ACACCATTCGCAAAAGCTCAGATTGGTCTCCAGAAGTACATTTAGAAGCTGAAGATAAG 420
QY	447 GCAATAGTGATACACATCTCTCTGGAAACAAAAGATAGTATTATGTCGGCTTTGGATG 506
Db	421 GCAATAGTGATACACATCTCTCTGGAAACAAAAGATAGTATTATGTCGGCTTTGGATG 480
QY	507 TTAAGCTTTACATATAGCTTACTTATCTGGAAAAAATCTCTCAGGTGTAGAAGAAAGGATT 566
Db	481 TTAAGCTTTNN 540
QY	567 GAAAAATATTTATCCAGACATAAAATTTATAAACTCTCACAGAGACTACTTATTGTCTA 626
Db	541 NNN 600
QY	627 AAAGTTAAAGCAGCACTACTTACGTCAATGGAAAAATTTGGTGCTATAGTCCAGTACATTGT 686
Db	601 NNN 660
QY	687 ATAAAGACCACAGTTGAAATGAACACTACCTCCACCAGAAAAATATAGAAGTCAGTCCAA 746
Db	661 NNN 720
QY	747 AATCAGAACTATGTTCTTAAATGGCATTTATACATATGCAAAACATGACCTTTCAAGTTCCAG 806
Db	721 NNN 780
QY	807 TGGCTCCACGCGCTTTTAAAGGAATCTCTGGAAACCAATTTGTATATAATGGAACAATA 866
Db	781 NNNNNNNCGCTTTTAAAGGAATCTCTGGAAACCAATTTGTATATAATGGAACAATA 840



AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.  
 TITLE HRI human cDNA project  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA project; 5'- and 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
 Location/Qualifiers  
 source  
 1. .807  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="OVARC1000513"  
 /tissue type="ovary, tumor tissue"  
 /clone lib="OVARC1"  
 /note="Vector: pME18SFL3"

ORIGIN  
 Query Match 55.9%; Score 750.8; DB 1; Length 807;  
 Best Local Similarity 99.4%; Pred. No. 1.7e-177;  
 Matches 774; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 558 GAAAGGATTGAAATATTATTTC-AGACATAAAATTTATTAACCTCCACGAGACTAC 616  
 DB 1 GAAAGGATTGAAATATTATTTCACAGACATATAAATTTATTAACCTCCACGAGACTAC 60  
 QY 617 TTATGTCTAAAGTAAAGCAGCAGCTACTTACGTCATGGAATTTGGTGTCTATAGTCC 676  
 DB 61 TTATGTCTAAAGTAAAGCAGCAGCTACTTACGTCATGGAATTTGGTGTCTATAGTCC 120  
 QY 677 AGTACATTGTATAAGACCAGTGTGAATATGAATCTACCTCCACGAGAAATATPAGAAT 736  
 DB 121 AGTACATTGTATAAGACCAGTGTGAATATGAATCTACCTCCACGAGAAATATPAGAAT 180  
 QY 737 CAGTGTCAAAATCAGAACTATGTTCTTAATGGATATACATATGCAACATGACCTT 796  
 DB 181 CAGTGTCAAAATCAGAACTATGTTCTTAATGGATATACATATGCAACATGACCTT 240  
 QY 797 TCAAGTTTCAGTGGCTCCACGCTTTTAAAGGAATCCTGGAAACCAATTTGTATAATG 856  
 DB 241 TCAAGTTTCAGTGGCTCCACGCTTTTAAAGGAATCCTGGAAACCAATTTGTATAATG 300  
 QY 857 GAAACAAATACCTGACTGTGAAATATGTCACCAATCTACCCAGTGTCTTTCTCAAAACGT 916  
 DB 301 GAAACAAATACCTGACTGTGAAATATGTCACCAATCTACCCAGTGTCTTTCTCAAAACGT 360  
 QY 917 TTTCCAAAAGGAATTTACCTTCCGCGTCAAGCATCTGATGAAATACACATCTTT 976  
 DB 361 TTTCCAAAAGGAATTTACCTTCCGCGTCAAGCATCTGATGAAATACACATCTTT 420  
 QY 977 TTGCTCTGAGAGATAAGTTTGTACTGAATACAGCTTTCTCTCTCCAGTCTT 1036  
 DB 421 TTGCTCTGAGAGATAAGTTTGTACTGAATACAGCTTTCTCTCTCCAGTCTT 480  
 QY 1037 TAACATTAGATCCCTTAGTGATTCATTCATATCTATATCGGTCTCCAAAACAGTCTGG 1096  
 DB 481 TAACATTAGATCCCTTAGTGATTCATTCATATCTATATCGGTCTCCAAAACAGTCTGG 540  
 QY 1097 AAACACGCTGTGATCCAGGATATPCCACTGATTTATGAATATTTTTCGGAAAACAC 1156  
 DB 541 AAACACGCTGTGATCCAGGATATPCCACTGATTTATGAATATTTTTCGGAAAACAC 600  
 QY 1157 TTCAATGCTGAGAGAAAAATTTTCGAGAAAAAATCTGATGTTACAGTTCCTTAATTGAA 1216

Db 601 TTCAATGCTGAGAGAAAAATTTTCGAGAAAAAATCTGATGTTACAGTTCCTTAATTGAA 660  
 QY 1217 ACCACTGACTGTATATTGTGAAAGCCAGACGACACACACCATGATGAAAGCTGAATAA 1276  
 Db 661 ACCACTGACTGTATATTGTGAAAGCCAGACGACACACACCATGATGAAAGCTGAATAA 720  
 QY 1277 AAGCAGTGTTTTGTAGTGACGCTGTATGTGAGAAAAAACAACC-AGGAAATACCTCTCAA 1334  
 Db 721 AAGCAGTGTTTTGTAGTGACGCTGTATGTGAGAAAAAACAACCAGGAATACCTCTCAA 779

RESULT 6  
 BG613775 820 bp mRNA linear EST 18-APR-2001  
 LOCUS 602639759F1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4770807 5', mRNA sequence.  
 DEFINITION  
 BG613775  
 ACCESSION  
 VERSION  
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 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1. (bases 1 to 820)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: L1CM1638 row: e column: 16  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue type="embryonal carcinoma"  
 /clone host="DH10B (T1 phage-resistant)"  
 /clone lib="NIH\_MGC 61"  
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 53.7%; Score 721.8; DB 2; Length 820;  
 Best Local Similarity 96.5%; Pred. No. 3.2e-170;  
 Matches 780; Conservative 0; Mismatches 23; Indels 5; Gaps 4;

QY 59 AGTCTCTGTCGCCCGTGGCCCATGGTGTTCGCGAGCCGAGTGAATAATCTAAA 118  
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 QY 119 ATCTCTCTCAAAAAGTAGAGGTGCGATCATAGATGACAACTTTATCTCTGAGGTGGAACAG 178  
 DB 61 ATCTCTCTCAAAAAGTAGAGGTGCGATCATAGATGACAACTTTATCTCTGAGGTGGAACAG 120

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QY 179 GAGCGATGAGTCTGTGTCGGGAATGAGACTTTTTCATTCGATTTATCAAAAACTGGGATGGA 238
Db 121 GAGCGATGAGTCTGTGTCGGGAATGAGACTTTTTCATTCGATTTATCAAAAACTGGGATGGA 180
QY 239 TAATTGGATAAATTTGTCGGGTGTCAGATATTTACTAGTACCAATGCAACTTTTCTTC 238
Db 181 TAATTGGATAAATTTGTCGGGTGTCAGATATTTACTAGTACCAATGCAACTTTTCTTC 240
QY 299 ACTCAAGCTCAATTTTATGAAGAAATTAATTCGATATAGAGCAGAGAAAGAAACAC 358
Db 241 ACTCAAGCTCAATTTTATGAAGAAATTAATTCGATATAGAGCAGAGAAAGAAACAC 300
QY 359 TTCTTCATGATGAGTTGACTCATTTACACCATTTTCGCAAAAGCTCAGATTTGCTCTCC 418
Db 301 TTCTTCATGATGAGTTGACTCATTTACACCATTTTCGCAAAAGCTCAGATTTGCTCTCC 360
QY 419 AGAAGTACATTTAGAGCTGAAGTAAGCAATAGTGATACACATCTCTCTCGGAACAAA 478
Db 361 AGAAGTACATTTAGAGCTGAAGTAAGCAATAGTGATACACATCTCTCTCGGAACAAA 420
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Db 421 AGATAGTGTATGTCGGCTTTGATGCTTTAAAGCTTTTACATATAGCTTACTTATCTGGAA 480
QY 539 AAACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTTATTCAGACATATAAATTTATAA 598
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QY 599 ACTCTACACGAGACTACTTTATGTCCTAAAGTTAAAGAGCAGCTACTTACGTCATGGAA 658
Db 541 AGTCTACACGAGACTACTTTATGTCCTAAAGTTAAAGAGCAGCTACTTACGTCATGGAA 600
QY 659 AATTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAACAGTTCGAAATGAACTACTCC 718
Db 601 AATCGGTGTCTATAGTCCAGTACATTTGATTAAGACCAACAGTTCGAAATGAACTACTCC 660
QY 719 ACCAGAAATATAGAGTCTAGTGTCCAAATTC-AGAACTATGTTCTT-AAATGGGATTA 775
Db 661 GACAGAAATATAGAGTCTAGTGTCCAAATTCAGAACTATGTTCTTACATGGGATTA 720
QY 776 TACATATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCTTTTAAAGAGGAATCC 835
Db 721 TACATATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCTTTTAAAGAGGAAT-C 779
QY 836 TGGAAACCTTTGATATAATGGAACAA 863
Db 780 TGGGAACCAATTGTTAAATGGAACAAA 807
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RESULT 7
BM457086
LOCUS
DEFINITION
  BM457086 918 bp mRNA linear EST 05-FEB-2002
  AGENCOURT_6411670 NIH_MGC_92 Homo sapiens cdna clone IMAGE:5583330
  5', mRNA sequence.
ACCESSION
  BM457086
VERSION
  BM457086.1 GI:18506126
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
  1 (bases 1 to 918)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabs-i@mail.nih.gov
  Tissue Procurement: ATCC
  cdna Library Preparation: Life Technologies, Inc.
  cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
  DNA sequencing by: Agencourt Bioscience Corporation
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
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High quality sequence stop: 636.  
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## ORIGIN

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Query Match 53.4%; Score 716.8; DB 3; Length 918;
Best Local Similarity 98.9%; Pred. No. 6e-169; 7; Indels 1; Gaps 1;
Matches 732; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 586 ATAAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAAGTTAAAGCAGCACTAC 645
Db 1 ATAAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAAGTTAAAGCAGCACTAC 60

QY 646 TTACGTCTGGAAGAAATTTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAACAG-TTGAA 704
Db 61 TTACGTCTGGAAGAAATTTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAACAGTAGAA 120

QY 705 AATGAACTACCTCCACGAGAAATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTT 764
Db 121 AATGAACTACCTCCACGAGAAATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTT 180

QY 765 AAATGGGATTTATACATATGCAACATGACCTTTTCAAGTTTCAGTGGCTCCACGCTTTTAA 824
Db 181 AAATGGGATTTATACATATGCAACATGACCTTTTCAAGTTTCAGTGGCTCCACGCTTTTAA 240

QY 825 AAAAGGAATCTCTGGAACCAATTTGTATAAATGGAACAAATACCTGCTGTAAGATGTC 884
Db 241 AAAAGGAATCTCTGGAACCAATTTGTATAAATGGAACAAATACCTGCTGTAAGATGTC 300

QY 885 AAAAATACCCAGTGTGTCTTCTCTCAAAAGCTTTTCCAAAAGGAATTTTACCTTCTCCGC 944
Db 301 AAAAATACCCAGTGTGTCTTCTCTCAAAAGCTTTTCCAAAAGGAATTTTACCTTCTCCGC 360

QY 945 GTACAAGCATCTGATGGAATTAACATCTTTTGTGCTGGAAGAGATAAAAGTTTGATACT 1004
Db 361 GTACAAGCATCTGATGGAATTAACATCTTTTGTGCTGGAAGAGATAAAAGTTTGATACT 420

QY 1005 GAAATACAAAGCTTTTCTACTTCTCTCCAGTCTTTTAAACATAGATCCCTTAGTGAATCATT 1064
Db 421 GAAATACAAAGCTTTTCTACTTCTCTCCAGGCTTTTAAACATAGATCCCTTAGTGAATCATT 480

QY 1065 CATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCTGTGATCCAGGATATCCA 1124
Db 481 CATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCTGTGATCCAGGATATCCA 540

QY 1125 CTGATTTATGAATTAATTTTGGGAAAAACACTTCAAAATGCTCAGAGAAAAAATTTATCGAG 1184
Db 541 CTGATTTATGAATTAATTTTGGGAAAAACACTTCAAAATGCTCAGAGAAAAAATTTATCGAG 600

QY 1185 AAAAAAATGATGTTTACAGTTCCTAAATTTGAAACCACTGATGATATTTGTTGTAAGGCC 1244
Db 601 AAAAAAATGATGTTTACAGTTCCTAAATTTGAAACCACTGATGATATTTGTTGTAAGGCC 660

QY 1245 AGAGCACACCATGATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGCCTGTATGT 1304
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Db	671	TAAACTCTACAGAGACTACTTATTGTCTAAAGTTAAAGCAGCACTACTTACGTATG	612
Qy	656	GAAAAATGGTGTCTATAGTCCAGTACATTTGTATAAGACACACAGTTGAAAATGAACCTACC	715
Db	611	GAAAAATGGTGTCTATAGTCCAGTACATTTGTATAAGACACACAGTTGAAAATGAACCTACC	552
Qy	716	TCCACGAGAAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTA	775
Db	551	TCCACGAGAAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTA	492
Qy	776	TACATATGCAAAATCATGACCTTTCAAGTTTCAGTGGCTCCAGCCCTTTTAAAAAGGAATCC	835
Db	491	TACATATGCAAAATCATGACCTTTCAAGTTTCAGTGGCTCCAGCCCTTTTAAAAAGGAATCC	432
Qy	836	TGGAACCACTTTGTATAAAATGGAACAAAATACCTGACTGTGAAAATGTCAAAATCACC	895
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Qy	896	GTGTGCTTCTCCCTCAAAACGTTTCCAAAAGGAATTTACCTTCTCCGCGTACAAAGCATC	955
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Qy	956	TGATGGAAATAACACATCTTTTGTCTGAGAGATAAAGTTTCATCTGAAAATCAACAGC	1015
Db	311	TGATGGAAATAACACATCTTTTGTCTGAGAGATAAAGTTTCATCTGAAAATCAACAGC	252
Qy	1016	TTTCTCTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTTCATATCTATAT	1075
Db	251	TTTCTCTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTTCATATCTATAT	192
Qy	1076	CGGTGCTCCAAAACAGTCTGGAACACAGCCTGTGATCCAGGATTTATCCATGATTTATGA	1135
Db	191	CGGTGCTCCAAAACAGTCTGGAACACAGCCTGTGATCCAGGATTTATCCATGATTTATGA	132
Qy	1136	AATTATTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATATCCAGAAAAAACTGA	1195
Db	131	AATTATTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATATCCAGAAAAAACTGA	72
Qy	1196	TGTTACAGTTCCTTAATTTT--GAAACCACTGACTCTATATTGTGTGAAAAGCCAGAGCAC	1253
Db	71	TGTTACAGTTCCTTAATTTTGGAAACCACTGACTCTATATTGTGTGAAAAGTTA--AACCCAG	13
Qy	1254	ACCATGGATGAA 1265	
Db	12	GCCATGGATGAA 1	
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			



Email: [genomics@hri.co.jp](mailto:genomics@hri.co.jp)  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

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Qy	1	CTCGAGGGATCTCGGGCGCTCCAGATGATGGTCGTCCTCTGGCGCGACGACCTTAG	60	
Db	15			
Qy	61	TGCTCGTCGCGTGGGGCCATGGGTGTGTGCCGACGCCGAGGTGGAAAAAATCTCAAAT	120	
Db	75			
Qy	121	CTCCTCAAAAAGTAGAGTGACATCATAGATGACAACTTTATCTCTGAGGTGGAAACGGA	180	
Db	135	CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCTGAGCGCGAACGGA	194	
Qy	181	GCATGAGTCTGTCTGGGAAATGTGACTTTTTCATTTCGATTATCAAAAAATCTGGGATGATA	240	
Db	195			
Qy	241	ATTGGATAAATGTCTCTGGGTGCAGAAATATTACTAGTACCAAAATGCAACTTTCTTCAC	300	
Db	255	ATTGGATAAATGTCTCTGGGTGTCTGAGAAATATGTCTAGTACCAAAATGCAACTTTCTTCAC	314	
Qy	301	TCAAGCTGAATGTTTATGAAAGAAATTAATTTGGGTATAAGCAGCAAGAAAGAAACACTT	360	
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Qy	361	CTTTCATGGTATGAGTTGACTCAATTTACACCATTTTCGCAAGCTCAGATTGGTCTCCAG	420	
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Qy	421	AAGTACATTTAGAGCTGAAGATTAAGCAATAGTGATACACATCTCTCTGGAAACAAAG	480	
Db	435	ARGTACATTTAGAAAGCTGAAGATTAAGCAATAGTGATACACATCTCTCTCTGGAAACAAAG	494	
Qy	481	ATAGTGTATTGTGGGCTTTCGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAA	540	
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Qy	541	ACTCTTCAGGTGTAGAAAGAAAGGATTCAAAATATTTATTCAGACATATAAATTTATAAC	600	
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Qy	601	TCTCACAGAGACTTACTTATTTGTTCTAAAGTTTAAAGC-AGCAGCTACTTACGTCTAT-CGAA	658	
Db	615	TCTCACAGAGACTTACTTATTTGTTCTAAAGTTTAAAGCAAGCAGCTACTTACGTCTATGGGA	674	
Qy	659	AATTGGTGTCTATAGTCCAGTACATTTGTAT-AAAGACACAG-TTGAAAAATGAACACTACCT	716	
Db	675	AATTGGTGTCTAAGTCCAAATACATCTGTATAAAGACCAAGTTTGAATAATGACTACCT	734	
Qy	717	CCACCA--GAAAATATAGAGTCAAGTGTCCAAATTCAGAACTA--TGTTCTTAAATGGGA	772	
Db	735	CCACCAAGAAAAATATANNAGTCAAGTGTCAAAAATTCAGAACTAATGTTTCTTAAATNGGG	794	
Qy	773	TTATACATATGC--AAACATGACCTTTCAAGTTCAGTGG--CTCCACGCGCTTTTAAAA	827	

Db	795	ATATNCATATTC	CAACATTG	ACCTTTCA	AGNTCAGT	GGGCTC	CAACNCCTTTT	TAAAAA	854
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ORGANISM	Homo sapiens	(human)							
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AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
TITLE	Mammalia; Euthalia; Euarchontoglires; Primates; Catarrhini;								
JOURNAL	Hominidae; Homo.								
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	National Institutes of Health, Mammalian Gene Collection (MGC)								
	Unpublished (1999)								
	Contact: Robert Strausberg, Ph.D.								
	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>								
	Tissue Procurement: ATCC								
	cdna Library Preparation: Life Technologies, Inc.								
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)								
	DNA Sequencing by: Agencourt Bioscience Corporation								
	Clone distribution: MGC clone distribution information can be								
	found through the I.M.A.G.E. Consortium/LNL at:								
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>								
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	Technologies."								
ORIGIN									
Query Match	50.6%	Score	680.2;	DB 3;	Length	938;			
Best Local Similarity	96.4%;	Pred.	No. 9.5e-160;						
Matches	706;	Conservative	0;	Mismatches	24;	Indels	2;	Gaps	1;
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Db	55	CTGGTGGATCTCGGCGGCTCC	CAGATGATGTCGTCTCTCGGGCGGCGACGACCCCTAG	114					
Qy	61	TGCTCGTCGCGGTGGGCGCCAT	TGGGTGTGTGCCAGCGCGCAGGTGGAAAAAATCTAAAT	120					
Db	115	TGCTCGTCGCGGTGGGCGCCAT	TGGGTGTGTGCCAGCGCGCAGGTGGAAAAAATCTAAAT	174					
Qy	121	CTCCTCAAAAGTAGAGGTGCA	CATCATGATGACAACTTTATCTGAGGTGGAAACAGGA	180					
Db	175	CTCCTCAAAAGTAGAGGTGCA	CATCATGATGACAACTTTATCTGAGGTGGAAACAGGA	234					
Qy	181	GCATGAGTCTGCGGGAATG	TGACATTTTTCATTTCGATTATCAAAAAATCTGGGATGGATA	240					
Db	235	GCATGAGTCTGCGGGAATG	TGACATTTTTCATTTCGATTATCAAAAAATCTGGGATGGATA	294					
Qy	241	ATTGGATAAAATGTCTGGGT	GTGAGAAATTTACTAGTACCAATGCAATTTTCTTCAC	300					



Db 295 ATTGATTAATTTGCTGGTGTGAGATATTAAGTACCAATGCACTTTTCTTCCAC 354  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATTAAGAGCGAGAAAGAAACACTT 360  
Db 355 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATTAAGAGCGAGAAAGAAACACTT 414  
Qy 361 CTTCATGATATGAGGTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTTGCTCTCCAG 420  
Db 415 CTTCATGATATGAGGTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTTGCTCTCCAG 474  
Qy 421 AAGTACATTTTGAAGCTGAAGATAGGCAATAGTGATACATCTCTCTCGAAACAAAG 480  
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Qy 661 TTGGTGCTATAGTCCAGTACATT--GTATTAAGACACAGTTGAAATGAATGAACTACCTCC 718  
Db 715 TTGGGTCTATAGTCCAGTACCTTTGGATATAAGAACCCAGTTTGAAATGAATGAACTACCTTC 774  
Qy 719 ACCAGAAATAT 730  
Db 775 CCCCCAAAAAT 786

RESULT 11  
LOCUS BG618347 784 bp mRNA linear EST 18-APR-2001  
DEFINITION 602645709P1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4767243 5',  
mRNA sequence.  
ACCESSION BG618347  
VERSION BG618347.1 GI:136669718  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 784)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>  
Plate: LLCM1629 row: a column: 04  
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SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and

FEATURES  
source

3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGGCCATTATGCCC-3', and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGGCGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	50.2%	Score	673.6	DB 2	Length	784			
Best Local Similarity	97.1%	Pred. No.	4.2e-158						
Matches	707	Conservative	0	Mismatches	19	Indels	2	Gaps	2

Qy 1 CTG CAGGATCTGCGGCGCTCCAGATGATGCTCTCTCTGCGCGGCGGACCCCTAG 60  
Db 51 CTGGTGGGATCTGCGGCGCTCCAGATGATGCTCTCTCTGCGCGGCGGACCCCTAG 110  
Qy 61 TGCTCGTCGCGGCGCTCCAGATGATGCTCTCTCTGCGCGGCGGACCCCTAG 120  
Db 111 TGCTCGTCGCGGCGCTCCAGATGATGCTCTCTCTGCGCGGCGGACCCCTAG 170  
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Qy 181 GCGATGATCTGTCGCGGAAATGCTTTTTCATTCGATATCAAAAAACTGGATGGATA 240  
Db 231 GCGATGATCTGTCGCGGAAATGCTTTTTCATTCGATATCAAAAAACTGGATGGATA 290  
Qy 241 ATTGGATAAAATTTCTCTGGGTGTCAGATATTTACTAGTACCATAATGCAACTTTTCTTCCAC 300  
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Qy 481 ATAGTGTTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540  
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Qy 660 ATTGCTGTCTATAGTCCAGTACATTTGATATAAGACACAGTTGA-AAATGAATCACTCTCC 718  
Db 711 ATGGTGTTCTATAGTCCAGTACATTTGATATAAGACACAGTTGAATGAATCACTCTCC 770  
Qy 719 ACCAGAAA 726  
Db 771 ACCAGAAA 778

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LOCUS CD109826  
DEFINITION AGENCOURT\_13889830 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:30345602 5', mRNA sequence.  
ACCESSION CD109826

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VERSION CD109826.1 GI:30754035
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rcgbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM383 row: m column: 03
High quality sequence stop: 489.
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ORIGIN
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QY 25 AGATGATGGTCTCTCTCTGGCGCGACGACCCCTAGTGTCTGTCGCGCGGCCCATGGG 84
DB 29 AGATGATGGTCTCTCTCTGGCGCGACGACCCCTAGTGTCTGTCGCGCGGCCCATGGG 88
QY 85 TGTGTCTCGGCGCGCGAGGTGGGAAAAATCTAAATCTCTCAAAAAGTAGAGTCGACA 144
DB 89 TGTGTCTCGGCGCGCGAGGTGGGAAAAATCTAAATCTCTCAAAAAGTAGAGTCGACA 148
QY 145 TCATAGATGACAACTTTATCTCTGAGGTGGGACAGGCGATGATCTGTCTGGGAATCTGA 204
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QY 205 CTTTTTCATTCGATTATCAAAAACTGGGATGGATAATTCGATAAAAAATTCGTGGGTGTC 264
DB 209 CTTTTTCATTCGATTATCAAAAACTGGGATGGATAATTCGATAAAAAATTCGTGGGTGTC 268
QY 265 AGAATATTACTAGTACCAATGCAACTTTCTTCACCTCAAGCTGAATGTTTATGAAGAA 324
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QY 325 TTAATTTGCGTATAGAGCAGAAAAAGAAACACTTCTCATGTGTAGGTGACTCAT 384
DB 329 TTAATTTGCGTATAGAGCAGAAAAAGAAACACTTCTTCATGTGTATGAGGTGACTCAT 388
QY 385 TTACACCATTTTCGCAAAAGCTCAGATTGGTCTCTCAGAAAGTACATTTAGAAAGCTGAAGATA 444

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Db 389 TTACACCATTTTCGCAAAAGCTCAGATTGGTCTCTCAGAAAGTACATTTAGAAAGCTCAAGATA 448
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QY 505 GTTTAAAGCTTTTACATATAGCTTACTTTATCTGGAAGAACTCTTCAGGTGTAGAAAGGA 564
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QY 625 TAAAGTTAAAGCAGCACTACTTACCTCAT-GGAAAATTTGGTCTCTATAGTCCAGTACAT 683
Db 629 TAAAGTTAAAGCAGCACTACTTACCTCTTTGGAAAAATTTGGTCTCTATAGTCCAGTACAT 688
QY 684 TGTATTAAGACCACTGTG-AAATGAACCTACCTCCACCAGAAAA 727
Db 689 TGGTTAAAGACCCAGTTGAAAAATGACTACCTCCCCCCAGAA 733
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LOCUS DKFZp781N1092.r1.781 (synonym: hlcc4) Homo sapiens cDNA clone
DEFINITION DKFZp781N1092.5', mRNA sequence.
ACCESSION BX956887
VERSION BX956887.1 GI:43442200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 674)
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
Mewes, H.W., Weil, B., Amid, C., Oeinger, A., Fobo, G., Han, M. and
Wiemann, S.
TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I.,
Wellenreuther, R., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center.
Heidelberg/Germany) within the cDNA sequencing consortium of the
German genome project.
No sl sequence available.
This clone (DKFZp781N1092) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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Qy 301 TCAAGCTGAATGTTTATGAGAAATTAATTAATGCGTATAGAGCAGAAAGAAACACTT 360
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Qy 361 CTTCATGTTATGAGTTCAGTCACTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420
Db 61 CTTCATGTTATGAGTTCAGTCACTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 120
Qy 421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTCGAACAAG 480
Db 121 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTCGAACAAG 180
Qy 481 ATAGTGTATGCGGCTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCGGAAA 540
Db 181 ATAGTGTATGCGGCTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCGGAAA 240
Qy 541 ACTCTTCAGGTGAGAGAAAGGATTGAAATATTTATTCAGACATATAATTTATAAC 600
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Qy 601 TCTCACAGAGACTACTTATTTGTTCTAAAGTTAAAGCAGCACTACTTACGTCATGGAAA 660
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Qy 661 TTGGTGTCTATAGTCCAGTACATTTGTATAAGACACAGATTGAAATGAACCTCCAC 720
Db 361 TTGGTGTCTATAGTCCAGTACATTTGTATAAGACACAGATTGAAATGAACCTCCAC 420
Qy 721 CAGAAATATAGAGTTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATATACAT 780
Db 421 CAGAAATATAGAGTTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATATACAT 480
Qy 781 ATGCAACATGACCTTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAGGAATCCTGGAA 840
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Qy 841 ACCATTTGTATAATGGAAACAAATACCTGACTGTGAAATGTCAAACCTACCGGTG 900
Db 541 ACCATTTGTATAATGGAAACAAATACCTGACTGTGAAATGTCAAACCTACCGGTG 600
Qy 901 TCTTTCTCAAAAGCTTTTCCAAAGCAATTTACTTCTCCGGTACAGCACTGATG 960
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Qy 961 GAAATACACATCTTT 976
Db 659 GAAATACACATCTTT 574
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RESULT 14
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LOCUS
DEFINITION DKFZp68612447_r1.686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp68612447_5', mRNA sequence.
ACCESSION AL707406
VERSION AL707406.1 GI:19690761
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 699)
Ottewaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and
Wiemann,S.
EST (Ottewaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and
Wiemann,S.)
JOURNAL Unpublished (2001)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
```

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by MediGenomix (Martinried/Germany) within the cDNA  
sequencing consortium of the German Genome Project. No sl sequence  
available.  
This clone (DKFZp68612447) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
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## ORIGIN

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Best Local Similarity 99.2%; Pred. No. 6.6e-148;  
Matches 636; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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Db 179 CTCCTCAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA 238  
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Qy 361 CTTCATGTTATGAGTTCAGTCACTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
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Qy 481 ATAGTGTATGCGGCTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCGGAAA 540  
Db 539 ATAGTGTATGCGGCTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCGGAAA 598  
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Db 659 TCTCACAGAGACTACTTATTTGTTCTAAAGTTAAAGCAGCA 699
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## RESULT 15

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CD697468  
LOCUS  
DEFINITION EST13991 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
EST 25-JUN-2003
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CD697468  
 CD697468.1 GI:32224985  
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 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominoidea; Homo.  
 REFERENCE  
 1 (bases 1 to 678)  
 Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and  
 Zeng,Y.-X.  
 TITLE  
 Transcriptional Gene Expression Profile of Human Nasopharynx  
 JOURNAL  
 Unpublished (2003)  
 COMMENT  
 Contact: Yixin Zeng  
 Cancer Center  
 Sun Yat-sen University  
 651 Dongfeng Road East, Guangzhou 510060, China  
 Tel: 86-1380-9770-743  
 Fax: 86-20-8775-4506  
 Email: yxzeng@gzsums.edu.cn.  
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 ORIGIN

## ORIGIN

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QY	61	TGCTCGTCGGCTGGGCGCCATGGGTGTGTCGCGAGCGCAGGTGGAAAAATCTAAAT	120	
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QY	121	CTCTCAAAAAGTAGAGTGCACATCATAGATGACACTTTATCCTGAGGTGGACACGGA	180	
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QY	181	GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTCATCAAAAACTGGGATGATA	240	
DB	211	GCGATGAGTCTGTCGGGAATGCAGCTTTTTCATTCGATTCATCAAAAACTGGGATGATA	270	
QY	241	ATTGGATAAAATTCCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTTCTTCAC	300	
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QY	301	TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACGACAGAAAAACAAT	360	
DB	331	TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACGACAGAAAAACAAT	390	
QY	361	CTTCATCGTATGAGTTGACTCATTTACACCATTTCCGCAAGCTCAGTTGGTCTCCAG	420	
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QY	541	ACTCTTCAGGTGTGAAGAAAGGATTCGAAAATATTTATTCAGACATAAAATTTTATAAC	600	

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 19:25:04 ; Search time 6920 Seconds

(without alignments)  
11031.901 Million cell updates/sec

Title: US-10-824-981-1

Perfect score: 1343

Sequence: 1 ctgcaggagatctgcggcgc.....ataccttaaatgagggtacc 1343

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.on.\*

5: gb.ov.\*

6: gb.pat.\*

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8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1343	100.0	1343	6 AR243657	AR243657 Sequence
5	1343	100.0	1343	6 AR580340	AR580340 Sequence
6	1334	99.3	1755	6 A26595	A26595 Human inter
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8	1334	99.3	1755	6 A76129	A76129 Sequence 3
9	1334	99.3	1755	6 AR243658	AR243658 Sequence
10	1334	99.3	1755	6 AR580341	AR580341 Sequence
11	1330.8	99.1	2755	6 CQ896434	CQ896434 Sequence
12	1330.8	99.1	2755	6 CS118026	CS118026 Sequence
13	1330.8	99.1	2755	6 AR380573	AR380573 Sequence
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16	1330.8	99.1	2784	6 AR030347	AR030347 Sequence
17	1330.8	99.1	2784	6 I93602	I93602 Sequence 1
18	1327.6	98.9	2069	8 AK222770	AK222770 Homo sapi

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20 1326 98.7 6099 6 CS119636
21 1324.4 98.6 1968 8 AK222812
22 1318.6 98.2 6741 6 AR491171
23 1171.4 87.2 1225 8 BC002590
24 1121.6 83.5 2147 8 AB169002
25 981.2 73.1 1629 6 CQ731750
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27 824.2 61.4 3284 4 BOVIFNRA
28 821 61.1 2914 4 OAU65978
29 819.8 61.0 1683 4 AB116561
30 819.4 61.0 2559 4 OAOIFNARE
31 625 46.5 4905 4 AF296666
32 540.2 40.2 3894 9 MUSIFNAR
33 538.6 40.1 2785 9 BC043935
34 538.6 40.1 3912 9 BC052429
35 537 40.0 3902 9 BC052217
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37 251.8 18.7 32906 8 HSIFNAR
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43 250.2 18.6 160344 8 AL954217
44 250.2 18.6 166547 8 AL954216
45 224.2 16.7 156045 14 AC144885

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#### ALIGNMENTS

#### RESULT 1

A26593 LOCUS A26593 1343 bp DNA linear PAT 02-OCT-1995  
DEFINITION Human interferon alpha receptor gene.  
ACCESSION A26593  
VERSION A26593.1 GI:1247458  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1343)

#### AUTHORS

TITLE WATER-SOLUBLE POLYPEPTIDES HAVING HIGH AFFINITY FOR INTERFERONS  
JOURNAL alpha AND beta  
PATENT: WO 9218626-A 17 29-OCT-1992;  
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AUTHORS Benoit, P. and Meyer, F.
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ACCESSION AR243657

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REFERENCE 1 (bases 1 to 1343)  
AUTHORS Bid.P., Gresser,I., Lutfalla,G., Meyer,F., Mogensen,K.E., Tovey,M. and Uze,G.  
TITLE Water-soluble polypeptides having a high affinity for .alpha. and beta. interferons  
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LOCUS	AR580340	1343 bp	DNA linear PAT 15-DEC-2004
DEFINITION	Sequence 1 from patent US 6787634.		
ACCESSION	AR580340		
VERSION	AR580340.1 GI:56610636		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1343)		
AUTHORS	Benoit,P., Meyer,F., Maguire,D., Plavec,I. and Tovey,M.G.		
TITLE	Isolated peptide or polypeptide of the extracellular portion of the human interferon receptor (IFN-R)		
JOURNAL	Patent: US 6787634-A 1 07-SEP-2004;		
	Medisup International, N.V.; Antilles;		
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LOCUS						
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A26595						
ACCESSION						
A26595.1						
VERSION						
GI:1247460						
KEYWORDS						
Homo sapiens (human)						
ORGANISM						
Homo sapiens						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;						
Hominidae; Homo.						
REFERENCE						
1 (bases 1 to 1755)						
WATER-SOLUBLE POLYPEPTIDES HAVING HIGH AFFINITY FOR INTERFERONS						
AUTHORS						
TITLE						
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JOURNAL						
Patent: WO 9218626-A 19 29-OCT-1992;						
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ORIGIN						
Query Match						
Best Local Similarity 99.3%; Score 1334; DB 6; Length 1755;						
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	CTGCAGGGATCTCGG	CGGGCTCCAGATGATG	TGTCCTCCTCGGGCGC	GACGACCCCTAG	60
Db	1	CTGCAGGGATCTCGG	CGGGCTCCAGATGATG	TGTCCTCCTCGGGCGC	GACGACCCCTAG	60
Qy	61	TGCTCGTCGGCGTGG	CGCCATGGGTGTTG	TCGCGAGCGCGAGGTG	GGAAAAATCTAAAT	120
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Qy	121	CTCCTCTAAAAGTAG	AGTCCACATCATAGAT	CACAACTTATCCTC	GAGTGGAAACAGGA	180
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181																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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## RESULT 7

A32391  
 LOCUS 1755 bp DNA linear PAT 08-JUL-1996  
 DEFINITION Interferon alpha and beta receptor gene.  
 ACCESSION A32391  
 VERSION A32391.1 GI:1567384

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo  
 1 (bases 1 to 1755)

## REFERENCE

AUTHORS  
 JOURNAL  
 FEATURES Patent: FR 2657881-A 20 09-AUG-1991;

Location/Qualifiers  
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 Db 1261 ATGAAAAAGCTGAATTAAGACGAGTGTGTTTATGAGCGCTGTATGTGAGAAAAACAAAC 1320  
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 Db 1321 GAAATACCTTAAA 1334

RESULT 8

A76129

LOCUS

1755 bp DNA linear PAT 19-OCT-1999

DEFINITION Sequence 3 from Patent W09320187.  
ACCESSION A76129  
VERSION A76129.1 GI:6088265  
KEYWORDS  
SOURCE unidentified  
ORGANISM  
unclassified  
unclassified sequences.  
REFERENCE 1 (bases 1 to 1755)  
Benoit,P. and Meyer,F.  
AUTHORS MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH  
TITLE NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON  
JOURNAL Patent: WO 9320187-A 3 14-OCT-1993;  
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)  
FEATURES  
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27. .1700  
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ORIGIN  
Query Match 99.3%; Score 1334; DB 6; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 6.2e-288;  
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1321 GAAATACCTCTAAA 1334

RESULT 9  
AR243658  
LOCUS AR243658  
DEFINITION Sequence 3 from patent US 6475983.  
ACCESSION AR243658  
VERSION AR243658.1 GI:27291032  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1755)  
AUTHORS Eid,P., Greaser,I., Lutfalla,G., Meyer,F., Mogensen,K.E., Tovey,M.  
and Uze,G.  
TITLE Water-soluble polypeptides having a high affinity for .alpha. and

.beta. interferons	
JOURNAL	Patent: US 6475983-A 3 05-NOV-2002;
ANX;	Medisup International N.V.; Curacao;
Location/Qualifiers	
source	1. .1755
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	/mol_type="mRNA"
ORIGIN	
Query Match 99.3%; Score 1334; DB 6; Length 1755;	
Best Local Similarity 100.0%; Pred. No. 6.2e-288;	
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 CTGCAGGATCTGCGCGGCTCCAGATGATGGTCTCTCTCGGGCGCAGCCCTAG 60
Qy	61 TGCTCGTCGCGCGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 120
Db	61 TGCTCGTCGCGCGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 120
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Db	301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACAGAGAAAGAAACACTT 360
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Qy	901 TCTTTCTCAAAAGCTTTTCCAAAAGGAATTTTACCTTCTCCGGTACAAAGCATCTGATG 960
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RESULT 10

AR580341

LOCUS AR580341 1755 bp DNA linear PAT 15-DEC-2004

DEFINITION Sequence 3 from patent US 6787634.

ACCESSION AR580341

VERSION AR580341.1 GI:56610637

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1755)

AUTHORS Benoit,P., Meyer,F., Maguire,D., Plavec,I. and Tovey,M.G.

TITLE Isolated peptide or polypeptide of the extracellular portion of the human interferon receptor (IFN-R)

JOURNAL Patent: US 6787634-A 3 07-SEP-2004;

Medisup International, N.V.; Antilles;

EPX;

FEATURES

source Location/Qualifiers

1. .1755

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 99.3%; Score 1334; DB 6; Length 1755;

Best Local Similarity 100.0%; Pred. No. 6.2e-288;

Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61 TGCTCGTCGCGCGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 120
Db	61 TGCTCGTCGCGCGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 120
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Qy	781 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGGAATCTTGAA 840
Db	781 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGGAATCTTGAA 840
Qy	841 ACCATTTGTATAATGGAAACAAATACCTGATGTGAAAAATGTCAAAATCTACCCAGGTG 900
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Db	1261	ATGAAAGCGCTGATATAAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAACAAAACCG	1320
Qy	1321	GAATACCTCTTAAA	1334
Db	1321	GAATACCTCTTAAA	1334
RESULT 11			
C0896434			
LOCUS	C0896434	2755 bp	DNA
DEFINITION	Sequence 258 from Patent WO2004076614.		
ACCESSION	C0896434		
VERSION	C0896434.1	GI:55468157	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1		
AUTHORS	Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Bruemendorf, T., Kinnemann, H., Roepcke, S., Hermann, K., Xinzhong, L., Pillarsky, C. and Staub, E.		
TITLE	Human nucleic acid sequences obtained from prostatic carcinomas		
JOURNAL	Patent: WO 2004076614-A 258 10-SEP-2004;		
	Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE); Specht, Thomas (DE); Schmitt, Armin (DE)		
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ORIGIN			
Query Match	99.1%;	Score 1330.8;	DB 6; Length 2755;
Best Local Similarity	99.9%;	Pred. No. 3.2e-287;	
Matches 1332;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	1	CTGCAGGATCTCGCGCGCTCCAGATGATGTCGTCCTCTGGGGGCGACACCGCTAG	60
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Qy	61	TGCTCGTCGCGGTGGGCCCATGGGTGTTGTCGCAGCCGCGAGGTGGAATAAATCTAAAT	120
Db	113	TGCTCGTCGCGGTGGGCCCATGGGTGTTGTCGCAGCCGCGAGGTGGAATAAATCTAAAT	172
Qy	121	CTCCTCAAAAGTAGAGGTGCGATCATAGATGACAACCTTTATCTCAGGTGGAACAGGA	180
Db	173	CTCCTCAAAAGTAGAGGTGCGATCATAGATGACAACCTTTATCTCAGGTGGAACAGGA	232
Qy	181	CGCATGAGTCTGCGGGAATGTGACCTTTTCATTGATATCAAAAACTGGGATGGATA	240
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Qy	241	ATTGGATAAAATTTGCTCGGTGTGCAATATTACTAGTACCAATGCAACTTTTCTTCAC	300
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Qy	301	TCAAGCTGAATGTTTATGAAGAAATTTAAATTCGGTATAAGAGCAGAAAAAGAAACACTT	360
Db	353	TCAAGCTGAATGTTTATGAAGAAATTTAAATTCGGTATAAGAGCAGAAAAAGAAACACTT	412
Qy	361	CTTCATGGTATGAGGTGTGACTCATTTACACCAATTCGAAAGCTCAGATGGTCTCCAG	420
Db	413	CTTCATGGTATGAGGTGTGACTCATTTACACCAATTCGAAAGCTCAGATGGTCTCCAG	472
Qy	421	AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG	480
Db	473	AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG	532
Qy	481	ATAGTCTTATGTGGGCTTTGGATGGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAAA	540



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Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATPACTGAAATACAAGCTTTCC 1020

Db 1013 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATPACTGAAATACAAGCTTTCC 1072

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Db 1073 TACTTCTCCAGTCTTTAAACATAGATCCCTTAGTGATTCATTCATATATATCGGTG 1132

Qy 1081 CTCCAAACAGCTCTGGAACACGCTGTGATCCAGGATTTCCAGTGAATTTATGAAATTA 1140

Db 1133 CTCCAAACAGCTCTGGAACACGCTGTGATCCAGGATTTCCAGTGAATTTATGAAATTA 1192

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Qy 1321 GAAATACCTCTAAA 1334

Db 1373 GAAATACCTCTAAA 1386

RESULT 12

CS118026

LOCUS CS118026 2755 bp DNA linear PAT 08-JUL-2005

DEFINITION Sequence 73 from Patent WO2005054508.

ACCESSION CS118026

VERSION CS118026.1 GI:70665972

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgate,R., Birnbaum,D. and Debono,S.

TITLE Gene expression profiling of colon cancer by dna microarrays and correlation with survival and histoclinical parameters

JOURNAL Patent: WO 2005054508-A 73 16-JUN-2005; Ipoogen (FR); Institut Paoli-Calmettes, Ipc (FR); Institut National de la Sante et de la Recherche Medicale (INSERM) (FR)

FEATURES

source Location/Qualifiers

1..2755

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/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/notes="Description of Artificial sequences:primer"

misc\_feature 1..2755

/notes="interferon (alpha, beta and omega) receptor 1(IFNAR1) gene."

ORIGIN

Query Match 99.1%; Score 1330.8; DB 6; Length 2755;

Best Local Similarity 99.9%; Pred. No. 3.2e-287;

Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 233 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATATCAAAAAAATCTGGATGATA 292

Qy 241 ATTGGATAAATATCTCGGGTGTGAGATATTACTAGTACCABATGCAACTTTTCTTCAC 300

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RESULT 14

HUMIFNRA

LOCUS Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA linear PRI 08-NOV-1994

DEFINITION cds.

ACCESSION J03171

VERSION J03171.1 GI:184645

KEYWORDS interferon-alpha receptor.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2755)

AUTHORS Use, G., Lutfalla, G. and Gresser, I.

TITLE Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA

JOURNAL Cell 60 (2), 225-234 (1990)

PUBMED 2153461

COMMENT Original source text: Human cell line DAUDI, cDNA to mRNA. Draft entry and computer-readable sequence for [1] kindly submitted by G. Use, 29-NOV-1989, for release after publication.

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/product="interferon-alpha receptor"

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Best Local Similarity 99.9%; Pred. No. 3.2e-287;

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DEFINITION human STS SHGC-35315, sequence tagged site.  
ACCESSION G28571  
VERSION G28571.1 GI:1408386  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2755)  
AUTHORS Myers,R.M.  
JOURNAL Unpublished (1996)  
COMMENT

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu

Primer A: TGACCAGAAATGAACCTGTGCA  
Primer B: TTTAAATAGTTAAGAGCTTGCCCG  
STS size: 175  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from J03171  
-- Washington University/Merck EST sequence.  
Location/Qualifiers  
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Best Local Similarity 99.9%; Pred. No. 3.2e-287;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

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Scoring table: IDENTITY NUC  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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8	1330.8	99.1	2755	3	US-09-949-016-101
9	1330.8	99.1	2784	2	US-08-471-454-1
10	1330.8	99.1	2784	2	US-08-466-974-1
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## ALIGNMENTS

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; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1343 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

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; LOCATION: 27..1334
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DB 841 ACCATTTGATAAATGAAACAAATACCTGACTGTGAAATGTCAAATCACTCCAGGTG 900
QY 901 TCTTTCTCAAAACGTTTTCAAAAGGAAATTTACCTTCTCCCGGTACAGCATCTGATG 960
DB 901 TCTTTCTCAAAACGTTTTCAAAAGGAAATTTACCTTCTCCCGGTACAGCATCTGATG 960

RESULT 2
US-07-971-834-1
; Sequence 1, Application US/07971834
; Patent No. 6475983
; GENERAL INFORMATION:
; APPLICANT: EID, Pierre
; APPLICANT: GRESSER, Ion
; APPLICANT: LUTFALLA, Georges
; APPLICANT: MEYER, Francois
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: TOVEY, Michael
; APPLICANT: UZE, Gilles
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
; AFFINITY FOR INTERFERONS ALPHA AND BETA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,834
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00318
; FILING DATE: 17-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:									
;	LENGTH:	1343 base pairs							
;	TYPE:	nucleic acid							
;	STRANDEDNESS:	single							
;	TOPOLOGY:	linear							
;	MOLECULE TYPE:	cdna							
;	FEATURE:								
;	NAME/KEY:	CDS							
;	LOCATION:	27..1334							
;	US-07-971-834-1								
Query Match 100.0%; Score 1343; DB 3; Length 1343;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CTGCAGGGATCTGCGGCGCTCCAGATGATGGTCTCTCTGGGGCGACGACCCCTAG	60						
Dd	1	CTGCAGGGATCTGCGGCGCTCCAGATGATGGTCTCTCTGGGGCGACGACCCCTAG	60						
Qy	61	TGCTCTGTCGGTGGGGCCCATGGGTGTTGTCGAGCGCGAGGTGGGAAAAAATCTAAAT	120						
Dd	61	TGCTCTGTCGGTGGGGCCCATGGGTGTTGTCGAGCGCGAGGTGGGAAAAAATCTAAAT	120						
Qy	121	CTCTCAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTCAGGTGGACACGGA	180						
Dd	121	CTCTCAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTCAGGTGGACACGGA	180						
Qy	181	GCATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAATCGGGATGGATA	240						
Dd	181	GCATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAATCGGGATGGATA	240						
Qy	241	ATTGGATAAAATTTGTCGGGTGTCAGAAATATTACTAGTACAAATGCAACTTTTCTTCAC	300						
Dd	241	ATTGGATAAAATTTGTCGGGTGTCAGAAATATTACTAGTACAAATGCAACTTTTCTTCAC	300						
Qy	301	TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACGAGAAAAGAAAACACTT	360						
Dd	301	TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACGAGAAAAGAAAACACTT	360						
Qy	361	CTTCATGGTATGAGTTGACTCATTTACACCATTTCCGAAAGCTCAGATTGGTCTCCAG	420						
Dd	361	CTTCATGGTATGAGTTGACTCATTTACACCATTTCCGAAAGCTCAGATTGGTCTCCAG	420						
Qy	421	AAGTACATTTAGAGCTGAAGATGAAGCAATAGTGATACACATCTCTCTGGAAACAAAG	480						
Dd	421	AAGTACATTTAGAGCTGAAGATGAAGCAATAGTGATACACATCTCTCTGGAAACAAAG	480						
Qy	481	ATAGTGTATATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAA	540						
Dd	481	ATAGTGTATATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAA	540						
Qy	541	ACTCTTCAGGTGTAGAAAGGAATTCGAAAATATTTATTCAGACATATAAATTTTATAAC	600						
Dd	541	ACTCTTCAGGTGTAGAAAGGAATTCGAAAATATTTATTCAGACATATAAATTTTATAAC	600						
Qy	601	TCTCACCAGAGACTACTTTATTTGCTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAA	660						
Dd	601	TCTCACCAGAGACTACTTTATTTGCTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAA	660						
Qy	661	TTGGTGTCTATAGTCCAGTACATTTGTATATAAGACACAGTTTGAATAATGAACCTCTCAC	720						
Dd	661	TTGGTGTCTATAGTCCAGTACATTTGTATATAAGACACAGTTTGAATAATGAACCTCTCAC	720						
Qy	721	CAGAAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTTAAATGGGATTATACAT	780						
Dd	721	CAGAAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTTAAATGGGATTATACAT	780						
Qy	781	ATGCAAACTAGCACTTTTCAAGTTCAGTGGCTCCACGGCTTTTTTAAAGGAATCTCTGAA	840						
Dd	781	ATGCAAACTAGCACTTTTCAAGTTCAGTGGCTCCACGGCTTTTTTAAAGGAATCTCTGAA	840						
Qy	841	ACCATTTGTATAAATGGAACAAATACTGACTGTGAAAATGTCAAAACTACCCAGTGTG	900						





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; APPLICATION NUMBER: US/07/971,834
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00318
; FILING DATE: 17-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1755 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 27..1697
; US-07-971-834-3

Query Match 99.3%; Score 1334; DB 3; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACGGGATCTGCGGCGGCTCCAGATGATGGTCTCTCGGCGGCGGCGGCGGCGGCTAG 60
Db 1 CTGACGGGATCTGCGGCGGCTCCAGATGATGGTCTCTCGGCGGCGGCGGCGGCGGCTAG 60

Qy 61 TGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 61 TGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120

Qy 121 CTCTCAAAAGTAGAGGTGCGATCATAGATGACATGATGATGATGATGATGATGATGATGAT 180
Db 121 CTCTCAAAAGTAGAGGTGCGATCATAGATGATGATGATGATGATGATGATGATGATGAT 180

Qy 181 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Db 181 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240

Qy 241 ATTGGATAAAATGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 241 ATTGGATAAAATGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300

Qy 301 TCAAGCTGAATGTTATGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
Db 301 TCAAGCTGAATGTTATGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360

Qy 361 CTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

Qy 421 AAGTACATTTAGAGCTGGAAGTAAGCAATAGTATGATGATGATGATGATGATGATGATGATG 480
Db 421 AAGTACATTTAGAGCTGGAAGTAAGCAATAGTATGATGATGATGATGATGATGATGATGATG 480

Qy 481 ATAGTGTATGCGGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 ATAGTGTATGCGGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

Qy 541 ACTCTTCAGGTGATGAAGAGGATGGAATATTTATTCAGACATATAATTTATTAATTAATTA 600
Db 541 ACTCTTCAGGTGATGAAGAGGATGGAATATTTATTCAGACATATAATTTATTAATTAATTA 600

Qy 601 TCTCACAGAGACTACTTATGCTTAAAGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 660
Db 601 TCTCACAGAGACTACTTATGCTTAAAGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 660
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## RESULT 6

US-09-240-675-3  
; Sequence 3, Application US/09240675  
; Patent No. 6787634

## GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,675  
FILING DATE:

PRIOR APPLICATION DATA: US/08/307,588  
FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA: EP 92400902.0  
FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1755 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

FEATURE:  
NAME/KEY: CDS

LOCATION: 27..1697  
US-09-240-675-3

Query Match 99.3%; Score 1334; DB 3; Length 1755;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGCAGGAGTCTGGCGGCTCCAGATGATGCTGCTCTCTGGGCGGACCCCTAG	60
Db	1	CTGCAGGAGTCTGGCGGCTCCAGATGATGCTGCTCTCTGGGCGGACCCCTAG	60
Qy	61	TGCTCGTCGCGCGGCGGCTGCTGCTGCGAGCGGAGGTGGAATAATCTAAAT	120
Db	61	TGCTCGTCGCGCGGCGGCTGCTGCTGCGAGCGGAGGTGGAATAATCTAAAT	120
Qy	121	CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGACAGGA	180
Db	121	CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGACAGGA	180
Qy	181	CGATGAGTCTGCGGAGATGACTTTTCATTCGATTAACAAAACCTGGATGGATA	240
Db	181	CGATGAGTCTGCGGAGATGACTTTTCATTCGATTAACAAAACCTGGATGGATA	240
Qy	241	ATTGGATAAATGCTCGGGTGCAGATATTAATAGTACCAATGCAACTTTCTTCAC	300
Db	241	ATTGGATAAATGCTCGGGTGCAGATATTAATAGTACCAATGCAACTTTCTTCAC	300
Qy	301	TCAAGCTGAATGTTTATGAAGAAATTAATTCGGTATAAGAGCAGAAAACACTT	360
Db	301	TCAAGCTGAATGTTTATGAAGAAATTAATTCGGTATAAGAGCAGAAAACACTT	360
Qy	361	CTTCATGATGAGGTGACTCATTTACACCAATTCGAAAAGCTGAGTTCCTCCAG	420
Db	361	CTTCATGATGAGGTGACTCATTTACACCAATTCGAAAAGCTGAGTTCCTCCAG	420
Qy	421	AAGTACATTTAGAGCTGAAGTAAGCAATAGTATACATCTCTCTCGAACAAAG	480
Db	421	AAGTACATTTAGAGCTGAAGTAAGCAATAGTATACATCTCTCTCGAACAAAG	480
Qy	481	ATAGTGTATGCGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGAAA	540
Db	481	ATAGTGTATGCGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGAAA	540
Qy	541	ACTCTTCAGGTGTAGAAGAAAGGATGAAAATATTTATTCAGACATAAAATTTATAAC	600

Db	541	ACTCTTCAGGTGTAGAAGAAAGGATGAAAATATTTATTCAGACATAAAATTTATAAC	600
Qy	601	TCTCACCAGAGACTACTTATGCTCTAAAAGTTAAAGCAGCACTACTTACGTCTGAAAA	660
Db	601	TCTCACCAGAGACTACTTATGCTCTAAAAGTTAAAGCAGCACTACTTACGTCTGAAAA	660
Qy	661	TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAAGTTGAAAATGAACCTCTCCAC	720
Db	661	TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAAGTTGAAAATGAACCTCTCCAC	720
Qy	721	CAGAAAATATAGAAGTCAAGTCTCAAAATCAGAACTATGTTCTTTAAATGGGATATACAT	780
Db	721	CAGAAAATATAGAAGTCAAGTCTCAAAATCAGAACTATGTTCTTTAAATGGGATATACAT	780
Qy	781	ATGCAAAACATGACCTTTTCAAGTTCAGTGGTCCACGGCTTTTAAAAAGGAATCTCGAA	840
Db	781	ATGCAAAACATGACCTTTTCAAGTTCAGTGGTCCACGGCTTTTAAAAAGGAATCTCGAA	840
Qy	841	ACCAATTTGATATAAGTGAACCAATACCTGACTGTGAAAATGTCAAACTACCCAGTGTG	900
Db	841	ACCAATTTGATATAAGTGAACCAATACCTGACTGTGAAAATGTCAAACTACCCAGTGTG	900
Qy	901	TCCTTCTCAAAAGCTTTTCCAAAAGCAATTTACCTTCTCCGGTCAAGCACTCTGATG	960
Db	901	TCCTTCTCAAAAGCTTTTCCAAAAGCAATTTACCTTCTCCGGTCAAGCACTCTGATG	960
Qy	961	GAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAAATCAAGCTTTCC	1020
Db	961	GAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAAATCAAGCTTTCC	1020
Qy	1021	TACTTCTCAGTCTTTAAACATTTAGATCCCTTAGTATTCATTCATATCTATATCGTG	1080
Db	1021	TACTTCTCAGTCTTTAAACATTTAGATCCCTTAGTATTCATTCATATCTATATCGTG	1080
Qy	1081	CTCCAAAACAGTCTGGAACACAGCGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA	1140
Db	1081	CTCCAAAACAGTCTGGAACACAGCGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA	1140
Qy	1141	TTTTTTGGGAAAAACACTTTCAAAATCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTA	1200
Db	1141	TTTTTTGGGAAAAACACTTTCAAAATCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTA	1200
Qy	1201	CAGTCTCTAATTTGAAACCACTGATGATATTTGTGTGAAAGCCAGAGACACACCATGG	1260
Db	1201	CAGTCTCTAATTTGAAACCACTGATGATATTTGTGTGAAAGCCAGAGACACACCATGG	1260
Qy	1261	ATGAAAAGCTGAATAAAGCAGTCTGTTTGTAGTACGCTGTATGTGAGAAAACAAACCAG	1320
Db	1261	ATGAAAAGCTGAATAAAGCAGTCTGTTTGTAGTACGCTGTATGTGAGAAAACAAACCAG	1320
Qy	1321	GAATACTCTCTAAA 1334	
Db	1321	GAATACTCTCTAAA 1334	

## RESULT 7

US-09-023-655-1118

; Sequence 1118, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA



ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2755 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g184645  
US-09-023-655-1118

Query Match 99.1%; Score 1330.8; DB 3; Length 2755;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCGAGGATCTCGCGGCTCCAGATGATGTCGTCCTCTGGGCGGACGACCTAG 60  
DB 53 CTGGTGGATCTCGCGGCTCCAGATGATGTCGTCCTCTGGGCGGACGACCTAG 112  
QY 61 TGTCTGTCGCGTGGGCCCATGGTGTTCGCGAGCGGAGGTGGAAAAATCTAAAT 120  
DB 113 TGTCTGTCGCGTGGGCCCATGGTGTTCGCGAGCGGAGGTGGAAAAATCTAAAT 172  
QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 180  
DB 173 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 232  
QY 181 GCGATGAGTCTGCGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGATGGATA 240  
DB 233 GCGATGAGTCTGCGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGATGGATA 292  
QY 241 ATTGGATAAATGTCCTGGGTGTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 300  
DB 293 ATTGGATAAATGTCCTGGGTGTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 352  
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
DB 353 TCAAGCTGAATGTTTATGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412  
QY 361 CTTTCATGATGAGTGTGACTTCATTTACACCATTTCCGAAGCTCAGATTGGTCTCCAG 420  
DB 413 CTTTCATGATGAGTGTGACTTCATTTACACCATTTCCGAAGCTCAGATTGGTCTCCAG 472  
QY 421 AAGTACATTTAGAGCTGAAGTAAGCAATAGTATGATACATCTCTCTCTGGAAACAAAAG 480  
DB 473 AAGTACATTTAGAGCTGAAGTAAGCAATAGTATGATACATCTCTCTCTGGAAACAAAAG 532  
QY 481 ATAGTGTATGTCGGCTTTCGATGCTTTTAACTTTTACATAGCTTACTTATCTCGAAA 540  
DB 533 ATAGTGTATGTCGGCTTTCGATGCTTTTAACTTTTACATAGCTTACTTATCTCGAAA 592  
QY 541 ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTTATTCAGACATAAAATTTATAAAC 600

DB 593 ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCAGACATAAAATTTATAAAC 652  
QY 601 TCTCACCAGAGACTACTTATTTCTAAAAGTTAAAGCAGCAGCTACTTACGTCTCATGGAAA 660  
DB 653 TCTCACCAGAGACTACTTATTTCTAAAAGTTAAAGCAGCAGCTACTTACGTCTCATGGAAA 712  
QY 661 TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAACAGTTGAAAATGAATCACTCCAC 720  
DB 713 TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAACAGTTGAAAATGAATCACTCCAC 772  
QY 721 CAGAAAATATAGAAGTCAAGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780  
DB 773 CAGAAAATATAGAAGTCAAGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 832  
QY 781 ATGCAACATGACCTTTCAAGTTCAAGTTCAGTGGCTCCACGCCCTTTTAAAGGAATCTCGAA 840  
DB 833 ATGCAACATGACCTTTCAAGTTCAAGTTCAGTGGCTCCACGCCCTTTTAAAGGAATCTCGAA 892  
QY 841 ACCATTGTATATAATGAAAACAAATACCTGACCTGTGAAAATGTCAAACTACCAGGTG 900  
DB 893 ACCATTGTATATAATGAAAACAAATACCTGACCTGTGAAAATGTCAAACTACCAGGTG 952  
QY 901 TCTTCTCTCAAAACGTTTTTCCAAAAGGAATTTACCTTCTCCGCTACAGCATCTGATG 960  
DB 953 TCTTCTCTCAAAACGTTTTTCCAAAAGGAATTTACCTTCTCCGCTACAGCATCTGATG 1012  
QY 961 GAAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAAATCAAGCTTTTC 1020  
DB 1013 GAAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAAATCAAGCTTTTC 1072  
QY 1021 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTG 1080  
DB 1073 TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTG 1132  
QY 1081 CTCAAAAACAGTCTGAAAACAGCCCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1140  
DB 1133 CTCAAAAACAGTCTGAAAACAGCCCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1192  
QY 1141 TTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTTATCGAGAAAACCTGATGTTA 1200  
DB 1193 TTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTTATCGAGAAAACCTGATGTTA 1252  
QY 1201 CAGTCTCTAAATTTGAAACCACTGACCTGATATTTGTGAAAGCCAGAGCACACCATGG 1260  
DB 1253 CAGTCTCTAAATTTGAAACCACTGACCTGATATTTGTGAAAGCCAGAGCACACCATGG 1312  
QY 1261 ATGAAAAGCTGAATAAAAGCAGTGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAACCAG 1320  
DB 1313 ATGAAAAGCTGAATAAAAGCAGTGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAACCAG 1372  
QY 1321 GAAATACCTCTAAA 1334  
DB 1373 GAAATACCTCTAAA 1386

## RESULT 8

US-09-949-016-101

; Sequence 101, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08



; NUMBER OF SEQ ID NOS: 207012									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 101									
; LENGTH: 2755									
; TYPE: DNA									
; ORGANISM: Human									
US-09-949-016-101									
Query Match									
Best Local Similarity 99.1%; Score 1330.8; DB 3; Length 2755;									
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	1	CTGCAGGAGTCTCGGGCGGCTCCACAGATGATGGTCCTCTCTGGCGCGGACCCCTAG	60						
Db	53	CTGTGGGATCTCGGGCGGCTCCACAGATGATGGTCCTCTCTGGCGCGGACCCCTAG	112						
Qy	61	TGCTCGTCGCGTCGGGCGCATGGGTGTTGTCCGACGCCGACAGTGGAAAAATCTAAAT	120						
Db	113	TGCTCGTCGCGTCGGGCGCATGGGTGTTGTCCGACGCCGACAGTGGAAAAATCTAAAT	172						
Qy	121	CTCTCTCAAAAGTAGAGGTGCACATCATAGATGACAACTTTATCTCTGAGGTGGAAACAGA	180						
Db	173	CTCTCTCAAAAGTAGAGGTGCACATCATAGATGACAACTTTATCTCTGAGGTGGAAACAGA	232						
Qy	181	GCAGTAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA	240						
Db	233	GCAGTAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA	292						
Qy	241	ATTGCGATAAAATGTCCTGGGTGTCAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC	300						
Db	293	ATTGCGATAAAATGTCCTGGGTGTCAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC	352						
Qy	301	TCRAGCTGAATGTTTATGGAAGAAATTTAAATTGCGTATTAAGAGCAGAAAAAGAAAAACCTT	360						
Db	353	TCRAGCTGAATGTTTATGGAAGAAATTTAAATTGCGTATTAAGAGCAGAAAAAGAAAAACCTT	412						
Qy	361	CTTCATGGTATGAGGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG	420						
Db	413	CTTCATGGTATGAGGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG	472						
Qy	421	AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG	480						
Db	473	AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG	532						
Qy	481	ATAGTGTATTGCGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTTCTGGAAAA	540						
Db	533	ATAGTGTATTGCGGCTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTTCTGGAAAA	592						
Qy	541	ACTCTTCAGGTGTAGAAGAAAGGATGAAAAATATTTATTCAGACATATAAAATTTATAAC	600						
Db	593	ACTCTTCAGGTGTAGAAGAAAGGATGAAAAATATTTATTCAGACATATAAAATTTATAAC	652						
Qy	601	TCTCACAGAGACTACTTATTGTCTTAAAGTTTAAAGCAGCCTACTTACGTCATCGAAAA	660						
Db	653	TCTCACAGAGACTACTTATTGTCTTAAAGTTTAAAGCAGCCTACTTACGTCATCGAAAA	712						
Qy	661	TTGGTGTCTATAGTCCAGTACATTTGTATATAAAGACCAAGTTGAAAAATGAACTTCCAC	720						
Db	713	TTGGTGTCTATAGTCCAGTACATTTGTATATAAAGACCAAGTTGAAAAATGAACTTCCAC	772						
Qy	721	CAGAAAAATATAGAGTCTAGTGTCCAAAAATCGAACTATATGTTCTTTAAATGGGATTTACAT	780						
Db	773	CAGAAAAATATAGAGTCTAGTGTCCAAAAATCGAACTATATGTTCTTTAAATGGGATTTACAT	832						
Qy	781	ATGCAAAATCATGACCTTTCAAGTTAGTGGCTCCAGCCCTTTTTTAAAGGAATCTCGNA	840						
Db	833	ATGCAAAATCATGACCTTTCAAGTTAGTGGCTCCAGCCCTTTTTTAAAGGAATCTCGNA	892						
Qy	841	ACCAATTTGTATAAATGGAAAAAATAATCTGACTGTGAAAAATGTCAAAACTACCCAGTGTG	900						
Db	893	ACCAATTTGTATAAATGGAAAAAATAATCTGACTGTGAAAAATGTCAAAACTACCCAGTGTG	952						
Qy	901	TCCTTCTCAAAAAGCTTTTTCAAAAAGGAAATTTACCTTCTCCGCGGTACAAGCATCTGATG	960						

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; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2784 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-471-454-1

Query Match      99.18; Score 1330.8; DB 2; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTG CAGGATCTGGGGGCTCCAGATGATGGTCCTCCCTGGGGCGGACGACCTAG 60
DB |||||
QY 53 CTGGTGGGATCTGGGGCGGCTCCAGATGATGGTCCTCCCTGGGGCGGACGACCTAG 112
DB |||||
QY 61 TGCTCGTCGCGTGGGCCCATGGGTGTGTCGCGAGCCGAGGTGGAAAAAATCTAAAT 120
DB |||||
QY 113 TGCTCGTCGCGTGGGCCCATGGGTGTGTCGCGAGCCGAGGTGGAAAAAATCTAAAT 172
DB |||||
QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGTGGAAACGGA 180
DB |||||
QY 173 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGTGGAAACGGA 232
DB |||||
QY 181 GCATGAGTCTGTCGGGAATGTGACTTTTTCATTTCGATTATCAAAAACCTGGATGGATA 240
DB |||||
QY 233 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTTCGATTATCAAAAACCTGGATGGATA 292
DB |||||
QY 241 ATTGGATAAAATGTCTGGGTGTGAGATATTAATAGTACCAAACTTTTCTTTTCCAC 300
DB |||||
QY 293 ATTGGATAAAATGTCTGGGTGTGAGATATTAATAGTACCAAACTTTTCTTTTCCAC 352
DB |||||
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATATGGGTATGAAGCAGAGAAAAAACAACCTT 360
DB |||||
QY 353 TCAAGCTGAATGTTTATGAAGAAATTAATATGGGTATGAAGCAGAGAAAAAACAACCTT 412
DB |||||
QY 361 CTTATCGGTATGAGTGTGACTTCATTACACCATTTTCGAAAGCTCAGATTGGTCTCCAG 420
DB |||||
QY 413 CTTATCGGTATGAGTGTGACTTCATTACACCATTTTCGAAAGCTCAGATTGGTCTCCAG 472
DB |||||
QY 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAAG 480
DB |||||
QY 473 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAAG 532
DB |||||
QY 481 ATAGTGTATGTGGCTTTCGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAA 540
DB |||||
QY 533 ATAGTGTATGTGGCTTTCGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAA 592
DB |||||
QY 541 ACTCTTCAGGTAGAGAAAGGATGAAATATTTATTCAGACATAAAATTTATAAAC 600
DB |||||
QY 593 ACTCTTCAGGTAGAGAAAGGATGAAATATTTATTCAGACATAAAATTTATAAAC 652
DB |||||
QY 601 TCTCACCAGAGACTACTTATTTGTCTAAAAGTTAAAGCAGCAGCTACTTACGTCTATGGA 660
DB |||||
QY 653 TCTCACCAGAGACTACTTATTTGTCTAAAAGTTAAAGCAGCAGCTACTTACGTCTATGGA 712
DB |||||
QY 661 TTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAAGTTGAAAAATGAATACCTCCAC 720
DB |||||
QY 713 TTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAAGTTGAAAAATGAATACCTCCAC 772
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QY 721 CAGAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGATTTATACAT 780
DB |||||
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QY 781 ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCACGCTTTTAAAAAGGAATCCTGGAA 840
DB |||||
QY 833 ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCACGCTTTTAAAAAGGAATCCTGGAA 892
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DB |||||
QY 893 ACCATTTGTATAAATGGAACCAAAATACCTGACTGTGAAAAATGTCAAACTACCCAGTGTG 952
DB |||||

RESULT 10
US-08-466-974-1
; Sequence 1, Application US/08466974
; Patent No. 5861258
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLIA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2784 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-466-974-1

Query Match 99.1%; Score 1330.8; DB 2; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCAGGATCTCGCGCGCTCCACAGATGATGGTCTCTCTGGCGCGCAGCCCTAG 60  
Db |||||  
Qy 53 CTGGTGGGATCTCGCGCGCTCCACAGATGATGGTCTCTCTGGCGCGCAGCCCTAG 112  
Db |||||  
Qy 61 TGCTCGTCCGCGTGGCGCCCATGGGTGTTGTCGCGCAGCGCAGGTGGAAAAATCTAAAT 120  
Db |||||  
Qy 113 TGCTCGTCCGCGTGGCGCCCATGGGTGTTGTCGCGCAGCGCAGGTGGAAAAATCTAAAT 172  
Db |||||  
Qy 121 CTCTCAAAAAAGTAGAGTGCACATCAGATGACAACTTTATCTGAGGTGGAAACAGGA 180  
Db |||||  
Qy 173 CTCTCAAAAAAGTAGAGTGCACATCAGATGACAACTTTATCTGAGGTGGAAACAGGA 232  
Db |||||  
Qy 181 GCGATGATCTGCGGGAATGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
Db |||||  
Qy 233 GCGATGATCTGCGGGAATGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 292  
Db |||||  
Qy 241 ATTGGATAAAATTTGTCGGGTGTCAGATAATTTACTAGTACCAATGCAAACTTTTCTTCCAC 300  
Db |||||  
Qy 293 ATTGGATAAAATTTGTCGGGTGTCAGATAATTTACTAGTACCAATGCAAACTTTTCTTCCAC 352  
Db |||||  
Qy 301 TCAAGCTGAATTTTATGAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360  
Db |||||  
Qy 353 TCAAGCTGAATTTTATGAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 412  
Db |||||  
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Qy 413 CTTCAATGATGAGTTGACTCATTTACCAATTTGCAAAAGCTCAGATTGGTCTCCAG 472  
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Qy 473 AAGTACATTTAGAGCTGAAGTAAAGCAATAGTATACATCTCTCTCGAACAAAG 532  
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Qy 593 ACTCTCAGGTGTAGAAGAAAGATTGAAATATTTATTTCCAGACATAAAATTTATAAC 652  
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Qy 601 TCTCACCAGACTACTTATTTGCTTAAAGTTAAAGCAGACTTACTACGTGATGGAATA 660  
Db |||||  
Qy 653 TCTCACCAGACTACTTATTTGCTTAAAGTTAAAGCAGACTTACTACGTGATGGAATA 712  
Db |||||  
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Db |||||  
Qy 833 ATGCAAAACATGACCTTTCAAGTTCAAGTCTCCAGCCCTTTTAAAAAGGAATCTCGAA 892  
Db |||||  
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Db |||||

Db 893 ACCATTTGTATAAATGGAAAAAATACTGACTGTGAAAAATGTCAAACTACCCAGTGTG 952  
Qy |||||  
Qy 901 TCTTTCTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGGGTCAAGCATCTGATG 960  
Db |||||  
Qy 953 TCTTTCTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGGGTCAAGCATCTGATG 1012  
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Qy 961 GAAATAACACATCTTTTGGTCTGAAAGATAAAGTTTGTATGATCTGAAATAAAGCTTTCC 1020  
Db |||||  
Qy 1013 GAAATAACACATCTTTTGGTCTGAAAGATAAAGTTTGTATGATCTGAAATAAAGCTTTCC 1072  
Db |||||  
Qy 1021 TACTTCTCTCCAGTCTTTAAACATTAAGTCCCTAGTATTCATTCATATCTATATCGGTG 1080  
Db |||||  
Qy 1073 TACTTCTCTCCAGTCTTTAAACATTAAGTCCCTAGTATTCATTCATATCTATATCGGTG 1132  
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Qy 1133 CTCCAAAAACAGTCTGGAAAAACAGCGCTGTGATCCAGGATTTCCACTGATTTTATGAAATTA 1192  
Db |||||  
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Qy 1193 TTTTGGGAAAAACACTTCAAAATCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252  
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Db |||||  
Qy 1253 CAGTCTCTAAATTTGAAACCACTGATGATATTTGTGTGAAAGCCAGACACACCATGG 1312  
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Qy 1261 ATGAAAAAGCTCAATAAAGCAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAAACAACCCAG 1320  
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Qy 1313 ATGAAAAAGCTCAATAAAGCAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAAACAACCCAG 1372  
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Qy 1321 GAAATACCTCTAAA 1334  
Db |||||  
Qy 1373 GAAATACCTCTAAA 1386  
Db |||||

RESULT 11

US-08-471-453-1  
; Sequence 1, Application US/08471453  
; Patent No. 5886153  
; GENERAL INFORMATION:  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: UZE, Gilles  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: GRESSER, Ion  
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
; NUMBER OF SEQUENCES: 2  
; PREPARATION OF THE CORRESPONDING PROTEIN  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P. C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U. S. A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,453  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/900,642  
; FILING DATE: 15-JUN-1992  
; APPLICATION NUMBER: FR 89/13770  
; FILING DATE: 20-OCT-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2784 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-471-453-1

Query Match 99.1%; Score 1330.8; DB 2; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCAGGGATCTCGCGGGCTCCAGATGATGTTGTCCTCTGGGGCGGACGACCTAG 60  
DB 53 CTGGTGGGATCTCGCGGGCTCCAGATGATGTTGTCCTCTGGGGCGGACGACCTAG 112  
QY 61 TGCTCGTGGCGTGGGCGGATGGGTGTTGTCGAGCGGCGGAGGTGGAAAAATCTAAAT 120  
DB 113 TGCTCGTGGCGTGGGCGGATGGGTGTTGTCGAGCGGCGGAGGTGGAAAAATCTAAAT 172  
QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCAGGTGGAAACAGGA 180  
DB 173 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCAGGTGGAAACAGGA 232  
QY 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTTCGATTATCAAAAACTGGGATGGATA 240  
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QY 241 ATTGGATAAAATTTGCTCGGGTGCAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC 300  
DB 293 ATTGGATAAAATTTGCTCGGGTGCAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC 352  
QY 301 TCAGCTGAATGTTTATGAGAAATTAATTTGCTGATTAAGAGCAGAAAGAAACACTT 360  
DB 353 TCAGCTGAATGTTTATGAGAAATTAATTTGCTGATTAAGAGCAGAAAGAAACACTT 412  
QY 361 CTTTCATGATGAGTTGACTCATTTACACCAATTTCCAAAGCTCAGATTGGCTCCAG 420  
DB 413 CTTTCATGATGAGTTGACTCATTTACACCAATTTCCAAAGCTCAGATTGGCTCCAG 472  
QY 421 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAACAAAAG 480  
DB 473 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAACAAAAG 532  
QY 481 ATAGTGTATGTCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540  
DB 533 ATAGTGTATGTCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 592  
QY 541 ACTCTCAGGTGTAGAAAGAGATTGAAATATTTATTCAGACATAAAATTTATAAAC 600  
DB 593 ACTCTCAGGTGTAGAAAGAGATTGAAATATTTATTCAGACATAAAATTTATAAAC 652  
QY 601 TCTCACCAGAGACTTACTTATGTTCTAAAGTTAAAGCAGCACTACTTACGTGATGGAATA 660  
DB 653 TCTCACCAGAGACTTACTTATGTTCTAAAGTTAAAGCAGCACTACTTACGTGATGGAATA 712  
QY 661 TTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAAGTTGAAATGAACCTCCTCCAC 720  
DB 713 TTGGTGTCTATAGTCCAGTACATTTGATTAAGACCAAGTTGAAATGAACCTCCTCCAC 772  
QY 721 CAGAAAAATATAGAAAGTCTGATGTTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
DB 773 CAGAAAAATATAGAAAGTCTGATGTTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 832  
QY 781 ATGCAAAATCATGACTTTTCAAGTTCAAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGGAA 840  
DB 833 ATGCAAAATCATGACTTTTCAAGTTCAAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGGAA 892

QY 841 ACCATTTGTATAAATGGAACCAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900  
DB 893 ACCATTTGTATAAATGGAACCAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 952  
QY 901 TCTTTCTCAAAAAGTTTTCCAAAAAGGAATTTACCTCTCCCGGTACCAAGCATCTGATG 960  
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QY 961 GAAATAACACATCTTTTCTGCTCTGAAAGATGAAAGTTTGATCTGAAATACAAGCTTTCC 1020  
DB 1013 GAAATAACACATCTTTTCTGCTCTGAAAGATGAAAGTTTGATCTGAAATACAAGCTTTCC 1072  
QY 1021 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1080  
DB 1073 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1132  
QY 1081 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTTACCTGATTTTATGAATTA 1140  
DB 1133 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTTATCCACTGATTTATGAATTA 1192  
QY 1141 TTTTGTGGGAACACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
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DB 1313 ATGAAAGCTGAATAAAAGCAGTGTGTTTGTAGTGAACGCTGTATGTGAGAAAAAACCAG 1372  
QY 1321 GAAATACCTCTAAA 1334  
DB 1373 GAAATACCTCTAAA 1386

RESULT 12  
US-09-949-016-2769  
; Sequence 2769, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE OF INVENTION: C0001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2769  
; LENGTH: 2753  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2769

Query Match 98.7%; Score 1326; DB 3; Length 2753;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1329; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTCAGGGATCTCGCGGGCTCCAGATGATGTTGTCCTCTGGGGCGGACGACCTAG 60  
DB 53 CTGGTGGGATCTCGCGGGCTCCAGATGATGTTGTCCTCTGGGGCGGACGACCTAG 112  
QY 61 TGCTCGTGGCGTGGGCGGATGGGTGTTGTCGAGCGGCGGAGGTGGAAAAATCTAAAT 120

Db 113 TGCTCGTGGCGTGGGCCATGGGTGTGTCCGACGCGCGAGGTGGAAAAATCTAAAT 172  
Qy 121 CTCTCAAAAGTAGAGTTCACATCATAGATGACAACTTTATCTCTGAGTGGGAACAGGA 180  
Db 173 CTCCTCAAAAGTAGAGTTCACATCATAGATGACAACTTTATCTCTGAGTGGGAACAGGA 232  
Qy 181 GCGATGAGTCTGTGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGATA 240  
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Qy 241 ATTGGATAAAATCTCTGGGTGTCAGATAATTTACTAGTACCAATGCAACTTTTCTTCAC 300  
Db 293 ATTGGATAAAATCTCTGGGTGTCAGATAATTTACTAGTACCAATGCAACTTTTCTTCAC 352  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 360  
Db 353 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 412  
Qy 361 CTTCACTGATAGAGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
Db 413 CTTCACTGATAGAGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 472  
Qy 421 AAGTACATTTAGAGCTGCAAGTAAGCAATAGTGTACACATCTCTCTGGACAAAAAG 480  
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Db 653 TCTCACCAGACACTTATTTGTCTAAAGTTAAAGCAGCACTACTTACGTCATGGA 712  
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Db 713 TTGTTGCTATAGTCCAGTACATTTGTATAAGACCAAGTTGAAATGAACTACTCTCAC 772  
Qy 721 CAGAAAAATAGAGTTCAGTCCAAATCAGAACTATGTTCTTAAATGGGATATACAT 780  
Db 773 CAGAAAAATAGAGTTCAGTCCAAATCAGAACTATGTTCTTAAATGGGATATACAT 832  
Qy 781 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTTAAAAAGGAATCTCGAA 840  
Db 833 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCCCTTTTAAAAAGGAATCTCGAA 892  
Qy 841 ACCATTTGTATATAGTGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900  
Db 893 ACCATTTGTATATAGTGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 952  
Qy 901 TCTTTCTCAAAAGCTTTTCCAAAGAAATTTACTCTTCGGCTCAAGCATCTGATG 960  
Db 953 TCTTTCTCAAAAGCTTTTCCAAAGAAATTTACTCTTCGGCTCAAGCATCTGATG 1012  
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATCAAGCTTTCC 1020  
Db 1013 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATCAAGCTTTCC 1072  
Qy 1021 TACTTCTCCAGTCTTTAAACATAGATCCCTTAGTGATTCATTCCATATCTATCCGTG 1080  
Db 1073 TACTTCTCCAGTCTTTAAACATAGATCCCTTAGTGATTCATTCCATATCTATATCCGTG 1132  
Qy 1081 CTCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1140  
Db 1133 CTCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1192  
Qy 1141 TTTTGTGGAAAAACACTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1193 TTTTGTGGAAAAACACTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252

Qy 1201 CAGTTCTTAATTTGAACCACTGACTGTATATTGTGTGAAGCCAGAGCACACCATGG 1260  
Db 1253 CAGTTCTTAATTTGAACCACTGACTGTATATTGTGTGAAGCCAGAGCACACCATGG 1312  
Qy 1261 ATGAAAAGCTGAATATAAAGCAGTGTGTTTATAGTACGCTGTATGTGAGAAAAACAAACCCAG 1320  
Db 1313 ATGAAAAGCTGAATATAAAGCAGTGTGTTTATAGTACGCTGTATGTGAGAAAAACAAACCCAG 1372  
Qy 1321 GAAATACCTCTAAA 1334  
Db 1373 GAAATACCTCTAAA 1386

## RESULT 13

US-09-056-461-21  
; Sequence 21, Application US/09056461  
; Patent No. 6713609  
; GENERAL INFORMATION:  
; APPLICANT: Chuntharapai, Anon  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Love, Richard B.  
; APPLICANT: Lu, Ji  
; APPLICANT: Stewart, Timothy A.  
; TITLE OF INVENTION: Type I Interferon Receptor Antibodies  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056.461  
; FILING DATE: 07-Apr-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/058212  
; FILING DATE: 16  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1039P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6741 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; US-09-056-461-21

Query Match 98.2%; Score 1318.6; DB 3; Length 6741;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 CTGAGGAGATCTGGGGCGGCTCCAGATGATGGTCTCTCTGGGGCGGAGACCCCTAG 60  
Db 12 CTGTGGGATCTGGGGCGGCTCCAGATGATGGTCTCTCTGGGGCGGAGACCCCTAG 71  
Qy 61 TGCTCGTCCGCTGGGCCCATGGGTGTTGTCGACAGCCGAGGTGGAATAATCTAAAAT 120  
Db 72 TGCTCGTCCGCTGGGCCCATGGGTGTTGTCGACAGCCGAGGTGGAATAATCTAAAAT 131  
Qy 121 CTCCTCAAAAAGTAGAGGTTCGACATCATAGATGACAACTTTTATCTCTGAGGTGGAACAGGA 180

Db 132 CTCTCAAAAAGTAGAGTCCACATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 191  
Qy 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGGATGGATA 240  
Db 192 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGGATGGATA 251  
Qy 241 ATTGGATAAAATTTGCTCGGGTGTGAGAAATTAATTTGGGTATAGAGCAGAAAAAACAACATT 360  
Db 252 ATTGGATAAAATTTGCTCGGGTGTGAGAAATTAATTTGGGTATAGAGCAGAAAAAACAACATT 311  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGGGTATAGAGCAGAAAAAACAACATT 360  
Db 312 TCAAGCTGAATGTTTATGAAGAAATTAATTTGGGTATAGAGCAGAAAAAACAACATT 371  
Qy 361 CTTTCATGATGAGTGTGACTTTTACACCAATTTGCGAAGCTCAGATTGGTCTCCAG 420  
Db 372 CTTTCATGATGAGTGTGACTTTTACACCAATTTGCGAAGCTCAGATTGGTCTCCAG 431  
Qy 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAAACAAAAG 480  
Db 432 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAAACAAAAG 491  
Qy 481 ATAGTGTATGTCGGCTTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA 540  
Db 492 ATAGTGTATGTCGGCTTTGGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA 551  
Qy 541 ACTCTCAGCTGTAGAGAAAGGATTTGAAAATATTTATCCAGACATATAAATTTATAAAC 600  
Db 552 ACTCTCAGCTGTAGAGAAAGGATTTGAAAATATTTATCCAGACATATAAATTTATAAAC 611  
Qy 601 TCTCACCAGAGACTACTTTATTTGCTAAAGTTAAAGCAGCACTACTTTACGTCATGGAAAA 660  
Db 612 TCTCACCAGAGACTACTTTATTTGCTAAAGTTAAAGCAGCACTACTTTACGTCATGGAAAA 671  
Qy 720 TTGGTGTCTATAGTCCAGTACATTTGTATTAAGACCAAGCTTTGAAAATGAACCTACCTCCAC 720  
Db 731 TTGGTGTCTATAGTCCAGTACATTTGTATTAAGACCAAGCTTTGAAAATGAACCTACCTCCAC 731  
Qy 780 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTTAAATGGGATTTATACAT 780  
Db 791 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTTAAATGGGATTTATACAT 791  
Qy 840 ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCACGGCTTTTAAAGAGGAATCCTGGAA 840  
Db 851 ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCACGGCTTTTAAAGAGGAATCCTGGAA 851  
Qy 900 ACCATTTGTATTAATGGAAAAACAATACCTGACTGTGAAAAATGTCAAAAACCTACCCAGTGTG 900  
Db 911 ACCATTTGTATTAATGGAAAAACAATACCTGACTGTGAAAAATGTCAAAAACCTACCCAGTGTG 911  
Qy 960 TCTTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGGGTACAGCATCTGATG 960  
Db 971 TCTTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGGGTACAGCATCTGATG 971  
Qy 1020 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGTACTGAAATACAAAGCTTTCC 1020  
Db 1031 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGTACTGAAATACAAAGCTTTCC 1031  
Qy 1080 TACTTCTCCAGTCTTTAACAATAGATCCCTTAGTGAATCAATTCATATATATCCGATG 1080  
Db 1091 TACTTCTCCAGTCTTTAACAATAGATCCCTTAGTGAATCAATTCATATATATCCGATG 1091  
Qy 1140 CTCCAAAACAGCTCGGAAACACGGCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1140  
Db 1151 CTCCAAAACAGCTCGGAAACACGGCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1151  
Qy 1200 TTTTTCGGAAAAACACTTCAAAATCCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1211 TTTTTCGGAAAAACACTTCAAAATCCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1211  
Qy 1260 CAGTTCCTAAATTTGAAACCACTGACTGATATTTGTGTGAAGCCAGAGCAACACCATGG 1260

Db 1212 CAGTTCCTAAATTTGAAACCACTGACTGTATATTTGTGTGAAGCCAGAGCAACACCATGG 1271  
Qy 1261 ATGAAAGCTGAATAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAACACAG 1320  
Db 1272 ATGAAAGCTGAATAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAACACAG 1331  
Qy 1321 GAAAT 1325  
Db 1332 GAAAT 1336  
  
RESULT 14  
US-09-949-016-11843  
; Sequence 11843, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11843  
; LENGTH: 35574  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-11843  
  
Query Match 18.7%; Score 251.8; DB 3; Length 35574;  
Best Local Similarity 76.9%; Pred. No. 9.2e-60;  
Matches 367; Conservative 0; Mismatches 12; Indels 98; Gaps 1;  
  
Qy 815 CGCTTTTAAAGGAATCCTCGGAAACCAATTTGTATTAATGGAAACAAATACCTGACTG 874  
Db 26115 CGCTTTTAAAGGAATCCTCGGAAACCAATTTGTATTAATGGAAACAAATACCTGACTG 26174  
Qy 875 TGAABATGTCAAACTACCCAGTGTCTTCTCTCAAAAGCTTTTCCAAAAGGAATTTA 934  
Db 26175 TGAABATGTCAAACTACCCAGTGTCTTCTCTCAAAAGCTTTTCCAAAAGGAATTTA 26234  
Qy 935 CTTTCTCCGGTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGGAAGAGATAAA 994  
Db 26235 CTTTCTCCGGTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGGAAGAGATAAA 26294  
Qy 995 GTTTGATCTGAAATACA----- 1012  
Db 26295 GTTTGATCTGAAATACAAGGTAAGGCAAGTGTGTTTACTGGAGATTGTAATTTCTCTGGT 26354  
Qy 1013 -----AGCT 1016  
Db 26355 GCAAGTTTTAAATTTGTTTTCTAAATGGAACATTAATTTCTTACAAATTTTTCTAGCT 26414  
Qy 1017 TTCTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCAATTCATATATATC 1076  
Db 26415 TTCTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCAATTCATATATATC 26474  
Qy 1077 GGTGCTCCAAAACAGCTGTGGAACAACGGCTGTGATCCAGGATTTATCCAGTATTTATGAA 1136  
Db 26475 GGTGCTCCAAAACAGCTGTGGAACAACGGCTGTGATCCAGGATTTATCCAGTATTTATGAA 26534  
Qy 1137 ATTATTTTGGGAAAAACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACT 1193  
Db 26535 ATTATTTTGGGAAAAACCTTCAAAATGCTGAGGTAAGAAAGACTGTATAGTATAAT 26591



## RESULT 15

US-09-949-016-14511  
; Sequence 14511, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14511  
; LENGTH: 35574  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14511

Query Match 18.7%; Score 251.8; DB 3; Length 35574;  
Best Local Similarity 76.9%; Pred. No. 9.2e-60;  
Matches 367; Conservative 0; Mismatches 12; Indels 98; Gaps 1;  
  
Qy 815 CGCCTTTTAAAGGAATCTCGAAACCATTTTGTATATAATGGAACAAATACCTGACTG 874  
Db 26115 CGCCTTTTAAAGGAATCTCGAAACCATTTGTTATATAATGGAACAAATACCTGACTG 26174  
  
Qy 875 TGAATAATGTCAAACTACCCAGTGTGTTCTTCAAAACGTTTTTCCAAAAGGAATTTA 934  
Db 26175 TGAATAATGTCAAACTACCCAGTGTGTTCTTCAAAACGTTTTTCCAAAAGGAATTTA 26234  
  
Qy 935 CTTTCTCCGGTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGAAGAGATAAA 994  
Db 26235 CTTTCTCCGGTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGAAGAGATAAA 26294  
  
Qy 995 GTTTGATACGAAATACA----- 1012  
Db 26295 GTTTGATACGAAATACAAGGTAAGGCAGTAGTTTACTGGAGATTGTAATCTCTGGT 26354  
  
Qy 1013 -----AGCT 1016  
Db 26355 GCAAGTTTTTAAATTTGTTTCTTAATTTGAACATATTTCTTTACAAATTTTTTCTAGCT 26414  
  
Qy 1017 TTCTACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076  
Db 26415 TTCTACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 26474  
  
Qy 1077 GGTGCTCCAAACAGCTCTGGAAACACGCTGTGATCCAGGATTTCCACTGATTTATGAA 1136  
Db 26475 GGTGCTCCAAACAGCTCTGGAAACACGCTGTGATCCAGGATTTCCACTGATTTATGAA 26534  
  
Qy 1137 ATTAATTTTTGGGAAACACATTTCAAATGCTCAGAGAAAAAATTTATCGAGAAAAAACT 1193  
Db 26535 ATTAATTTTTGGGAAACACATTTCAAATGCTCAGGTAAGAAAGACTGTATAGTATATT 26591

Search completed: January 17, 2006, 23:26:06  
Job time : 270 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:10:37 ; Search time 32.8172 Seconds  
(without alignments)  
1098.405 Million cell updates/sec

Title: US-10-824-981-2

Perfect score: 2313

Sequence: 1 MGVLLGATTVLVAVGPWV.....KSSVFSDAVCEKTPGNTSK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgm2\_6/ptodata/1/iaa/5 COMB pep:\*
- 2: /cgm2\_6/ptodata/1/iaa/6 COMB pep:\*
- 3: /cgm2\_6/ptodata/1/iaa/H COMB pep:\*
- 4: /cgm2\_6/ptodata/1/iaa/PCTUS COMB pep:\*
- 5: /cgm2\_6/ptodata/1/iaa/RE COMB pep:\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles1 pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2313	100.0	436	1	US-08-307-588-2
2	2313	100.0	436	2	US-07-971-834-2
3	2313	100.0	436	2	US-09-240-675-2
4	2313	100.0	557	1	US-08-328-256-10
5	2313	100.0	557	1	US-08-471-454-2
6	2313	100.0	557	1	US-08-466-974-2
7	2313	100.0	557	1	US-08-471-453-2
8	2313	100.0	557	1	US-08-307-588-4
9	2313	100.0	557	2	US-07-971-834-4
10	2313	100.0	557	2	US-09-240-675-4
11	2313	100.0	557	2	US-09-949-016-5372
12	2304	99.6	575	2	US-09-949-016-8640
13	2265	97.9	434	1	US-08-328-256-11
14	2265	97.9	496	1	US-08-328-256-12
15	2158	93.3	631	2	US-09-056-461-22
16	1172	50.7	224	2	US-08-871-572B-9
17	1141	49.3	226	2	US-08-871-572B-10
18	781.5	33.8	224	2	US-08-871-572B-13
19	720.5	31.2	227	2	US-08-871-572B-14
20	588.5	25.4	224	2	US-08-871-572B-11
21	490.5	21.2	202	4	PCT-US94-14277-3
22	480.5	20.8	219	2	US-08-871-572B-12
23	465.5	20.2	200	4	PCT-US94-14277-4
24	228.5	9.9	233	2	US-08-871-572B-8
25	228.5	9.9	273	2	US-09-949-016-11056
26	228.5	9.9	325	1	US-08-683-743-4
27	228.5	9.9	325	2	US-09-870-574-3

Query Match 100.0% Score 2313; DB 1; Length 436;

28	228.5	9.9	325	2	US-09-265-540E-6	Sequence 6, Appli
29	214	9.3	199	2	US-10-090-365-35	Sequence 35, Appl
30	214	9.3	199	2	US-09-728-911-35	Sequence 35, Appl
31	203	8.8	332	4	PCT-US94-14277-2	Sequence 2, Appli
32	200	8.6	567	2	US-09-949-016-11502	Sequence 11502, A
33	198	8.6	553	1	US-08-943-087-2	Sequence 2, Appli
34	198	8.6	553	1	US-08-943-087-14	Sequence 14, Appl
35	198	8.6	553	1	US-08-943-087-16	Sequence 16, Appl
36	198	8.6	553	1	US-08-943-087-18	Sequence 18, Appl
37	198	8.6	553	1	US-08-943-087-20	Sequence 20, Appl
38	198	8.6	553	1	US-08-943-087-22	Sequence 22, Appl
39	198	8.6	553	1	US-08-943-087-24	Sequence 24, Appl
40	198	8.6	553	1	US-08-943-087-26	Sequence 26, Appl
41	198	8.6	553	1	US-08-943-087-28	Sequence 28, Appl
42	198	8.6	553	1	US-08-943-087-30	Sequence 30, Appl
43	198	8.6	553	1	US-08-943-087-32	Sequence 32, Appl
44	198	8.6	553	1	US-08-943-087-34	Sequence 34, Appl
45	198	8.6	553	1	US-08-943-087-36	Sequence 36, Appl

#### ALIGNMENTS

RESULT 1  
US-08-307-588-2  
; Sequence 2, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: FLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 436 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-307-588-2

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Best Local Similarity 100.0%; Pred. No. 9.2e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVVLGATTLVLVAVGPWVLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESVCNVT 60
Db 1 MMVVLGATTLVLVAVGPWVLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESVCNVT 60
Qy 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120
Db 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120
Qy 121 TPRKQAGIPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTSYLLIWNSSGVEERI 180
Db 121 TPRKQAGIPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTSYLLIWNSSGVEERI 180
Qy 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Db 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Qy 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
Qy 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Qy 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Qy 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 2
US-07-971-834-2
; Sequence 2, Application US/07971834
; Patent No. 6475983
; GENERAL INFORMATION:
; APPLICANT: EID, Pierre
; APPLICANT: GRESSER, Ion
; APPLICANT: LUTFALLA, Georges
; APPLICANT: MEYER, Francois
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: TOVEY, Michael
; APPLICANT: UZE, Gilles
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
; AFFINITY FOR INTERFERONS ALPHA AND BETA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/07/971,834
; APPLICATION NUMBER: 17-FEB-1993
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00318
; FILING DATE: 17-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-971-834-2

Query Match 100.0%; Score 2313; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.2e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVVLGATTLVLVAVGPWVLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESVCNVT 60
Db 1 MMVVLGATTLVLVAVGPWVLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESVCNVT 60
Qy 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120
Db 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120
Qy 121 TPRKQAGIPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTSYLLIWNSSGVEERI 180
Db 121 TPRKQAGIPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTSYLLIWNSSGVEERI 180
Qy 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Db 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Qy 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
Qy 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Qy 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Qy 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 3
US-09-240-675-2
; Sequence 2, Application US/09240675
; Patent No. 6787634
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; TITLE OF INVENTION: INTERFERON
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,675  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 436 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-240-675-2

Query Match 100.0%; Score 2313; DB 2; Length 436;  
Best Local Similarity 100.0%; Pred. No. 9,2e-230;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGKNLSPKQVEVDIIDDNFILRNWRSDESVDNF 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGKNLSPKQVEVDIIDDNFILRNWRSDESVDNF 60  
Qy 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPTTCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPTTCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANNMTFOVQWLHAFLEKPNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVYLKWDYTYANNMTFOVQWLHAFLEKPNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKOSGNT 360  
Db 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKOSGNT 360  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 4

US-08-328-256-10  
Sequence 10, Application US/08328256  
Patent No. 5643749  
GENERAL INFORMATION:  
APPLICANT: REVEL, Michel  
APPLICANT: ABRAMOVICH, Carolina  
APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERPERON ALPHA-RECEPTOR, ITS  
TITLE OF INVENTION: PREPARATION AND USE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/328,256  
FILING DATE: 24-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107378  
FILING DATE: 24-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: REVEL=13  
REFERENCE/DOCKET NUMBER: 25,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-328-256-10

Query Match 100.0%; Score 2313; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGKNLSPKQVEVDIIDDNFILRNWRSDESVDNF 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGKNLSPKQVEVDIIDDNFILRNWRSDESVDNF 60  
Qy 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPTTCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPTTCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANNMTFOVQWLHAFLEKPNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVYLKWDYTYANNMTFOVQWLHAFLEKPNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKOSGNT 360  
Db 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKOSGNT 360  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

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RESULT 5
US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-229;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESVGNVT 60
Db 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESVGNVT 60
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Db 61 FSDPYQKTGMNDWIKLSGQNITSTKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Qy 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEIRI 180
Db 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEIRI 180
Qy 181 ENIYSRHKIYKLSPTTYCLKVKAALTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPTTYCLKVKAALTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240

241 NONYLKWDTYTYANMTFQVQWLHAFILKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFOK 300
241 NONYLKWDTYTYANMTFQVQWLHAFILKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFOK 300
301 GIYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360
301 GIYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360
361 VIQDYPLIYEIIFWNTSNAERKIEBKTDVTPVNLKPLTVYCVKARAHMTDEKLKSSV 420
361 VIQDYPLIYEIIFWNTSNAERKIEBKTDVTPVNLKPLTVYCVKARAHMTDEKLKSSV 420
421 FSDAVCEKTKPGNTSK 436
421 FSDAVCEKTKPGNTSK 436

RESULT 6
US-08-466-974-2
; Sequence 2, Application US/08466974
; Patent No. 5861258
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-974-2

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-229;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESVGNVT 60
Db 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESVGNVT 60
Qy 61 FSDPYQKTGMNDWIKLSGQNITSTKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Db 61 FSDPYQKTGMNDWIKLSGQNITSTKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Qy 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEIRI 180
Db 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEIRI 180
Qy 181 ENIYSRHKIYKLSPTTYCLKVKAALTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPTTYCLKVKAALTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240
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Db 61 FSDYQKTGMDNWKLSGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVWALDGLSFYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVWALDGLSFYSLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPETTYCLVKVAALTSWKIGYVSPVHCITTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLVKVAALTSWKIGYVSPVHCITTVENELPPENIEVSQ 240  
Qy 241 NQNTVLKWDITYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTCVFFQNVFQK 300  
Db 241 NQNTVLKWDITYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTCVFFQNVFQK 300  
Qy 301 GYLLRVOASDGNNTSPWSEIEKFDTEIQAFLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Db 301 GYLLRVOASDGNNTSPWSEIEKFDTEIQAFLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTVYCVKARHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTVYCVKARHTMDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 7

US-08-471-453-2  
; Sequence 2, Application US/08471453  
; Patent No. 5886153  
; GENERAL INFORMATION:  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: UZE, Gilles  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: GRESSER, Ion  
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P. C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,453  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/900,642  
; FILING DATE: 15-JUN-1992  
; APPLICATION NUMBER: FR 89/13770  
; FILING DATE: 20-OCT-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 960-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100

; TELEX: 200797 NLXN UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-453-2

Query Match 100.0%; Score 2313; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVLVAVGPVLSAAAGGKLNKSPKQVEVDIIDDNFILRWRSDSVGNVT 60  
Db 1 MMVLLGATTLVLVAVGPVLSAAAGGKLNKSPKQVEVDIIDDNFILRWRSDSVGNVT 60  
Qy 61 FSDYQKTGMDNWKLSGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMDNWKLSGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVWALDGLSFYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVWALDGLSFYSLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPETTYCLVKVAALTSWKIGYVSPVHCITTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLVKVAALTSWKIGYVSPVHCITTVENELPPENIEVSQ 240  
Qy 241 NQNTVLKWDITYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTCVFFQNVFQK 300  
Db 241 NQNTVLKWDITYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTCVFFQNVFQK 300  
Qy 301 GYLLRVOASDGNNTSPWSEIEKFDTEIQAFLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Db 301 GYLLRVOASDGNNTSPWSEIEKFDTEIQAFLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTVYCVKARHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTVYCVKARHTMDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 8

US-08-307-588-4  
; Sequence 4, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:

✓ Appl

APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-307-588-4

Query Match 100.0%; Score 2313; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGVT 60  
DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGVT 60  
QY 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEAEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
DB 121 TPFRKAQIGPPEVHLEAEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 QNYVLKWDYTYANMTFQVQWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 QNYVLKWDYTYANMTFQVQWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
QY 421 FSDAVCEKTPGNTSK 436  
DB 421 FSDAVCEKTPGNTSK 436

RESULT 9

US-07-971-834-4  
Sequence 4, Application US/07971834  
Patent No. 6475983  
GENERAL INFORMATION:  
APPLICANT: Eid, Pierre  
APPLICANT: GRESSER, Ion  
APPLICANT: LUTFALLA, Georges  
APPLICANT: MEYER, Francois  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: TOVEY, Michael  
APPLICANT: UZE, Gilles  
TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH

TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,834  
FILING DATE: 17-FEB-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR91/00318  
FILING DATE: 17-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: EID=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-971-834-4

Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGVT 60  
DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGVT 60  
QY 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEAEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
DB 121 TPFRKAQIGPPEVHLEAEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 QNYVLKWDYTYANMTFQVQWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 QNYVLKWDYTYANMTFQVQWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
QY 421 FSDAVCEKTPGNTSK 436  
DB 421 FSDAVCEKTPGNTSK 436

RESULT 10  
US-09-240-675-4  
; Sequence 4, Application US/09240675  
; Patent No. 6787634  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (RPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,675  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-240-675-4

Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVAVGFWLSAAAGGNLKSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVAVGFWLSAAAGGNLKSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Qy 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Qy 181 ENISVRHKIYKLSPTTTCVLAQKALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISVRHKIYKLSPTTTCVLAQKALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNTVLLKWDYTYANNMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
Db 241 NQNTVLLKWDYTYANNMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Qy 241 NQNTVLLKWDYTYANNMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300

Db 241 NQNTVLLKWDYTYANNMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 11  
US-09-949-016-5972  
; Sequence 5972, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: RastSEQ for Windows Version 4.0  
; SEQ ID NO 5972  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5972

Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVAVGFWLSAAAGGNLKSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVAVGFWLSAAAGGNLKSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Qy 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Qy 181 ENISVRHKIYKLSPTTTCVLAQKALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISVRHKIYKLSPTTTCVLAQKALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNTVLLKWDYTYANNMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
Db 241 NQNTVLLKWDYTYANNMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTPNLKPLTYVCVKARAHMTWDEKLNKSSV 420



Db 421 FSDAVE 427  
|||||  
301 GIYLLRVQASDGNNTSFWSBEIKFTDTETQAFLLPPVFNIRSLSDSFHYIIGAPKOSGNTP 360  
301 GIYLLRVQASDGNNTSFWSBEIKFTDTETQAFLLPPVFNIRSLSDSFHYIIGAPKOSGNTP 360  
361 VIQYPLIYELIFWENTSNARKEIKKTDVTVNPKPLTVYCVKARAHWTWDEKLNKSSV 420  
361 VIQYPLIYELIFWENTSNARKEIKKTDVTVNPKPLTVYCVKARAHWTWDE----- 413  
421 FSDAVE 427  
414 -SDAVE 419  
RESULT 15  
US-09-056-461-22  
; Sequence 22, Application US/09056461  
; Patent No. 6713609  
; GENERAL INFORMATION:  
; APPLICANT: Chunharapai, Anon  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Love, Richard B.  
; APPLICANT: Lu, Ji  
; APPLICANT: Stewart, Timothy A.  
; TITLE OF INVENTION: Type I Interferon Receptor Antibodies  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056.461  
; FILING DATE: 07-Apr-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/058212  
; FILING DATE: 16  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1039P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 631 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-056-461-22  
Query Match 93.3%; Score 2158; DB 2; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1.7e-213;  
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 30 LKSPQKVEVDIIDNFIILNRNRSDESVGNVTFSDYQKTMNDNKLKSGCNITSTKCNF 89  
Db 1 LKSPQKVEVDIIDNFIILNRNRSDESVGNVTFSDYQKTMNDNKLKSGCNITSTKCNF 60  
QY 90 SSLKLVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPVEHLEADKAIIVHISPG 149  
Db 61 SSLKLVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPVEHLEADKAIIVHISPG 120  
QY 150 TKDSVMWALDGLSFTYSLLIWKNSSGVEERIENYSRHKIYKLPETTYCLKKAALTS 209  
|||||  
US-08-328-256-12  
; Sequence 12, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel  
; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 496 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-328-256-12  
Query Match 95.7%; Score 2213; DB 1; Length 496;  
Best Local Similarity 98.1%; Pred. No. 2.4e-219;  
Matches 419; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
QY 1 MNVLLGATTLVLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNRSDESVGNVT 60  
Db 1 MNVLLGATTLVLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNRSDESVGNVT 60  
QY 61 FSPDYQKTMNDNKLKSGCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTMNDNKLKSGCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPVHLEADKATVIHISPTGKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPVHLEADKATVIHISPTGKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
QY 181 ENIYSRHKIYKLPETTYCLKKAALTSWKIGVYSPVHCIKTTVENELPPPEIEVSQ 240  
Db 181 ENIYSRHKIYKLPETTYCLKKAALTSWKIGVYSPVHCIKTTVENELPPPEIEVSQ 240  
QY 241 NONYVLKWDYTYANNMTFQVQMLHAFKRNPGNHLKYKQIIPDCENVTTCQVFPQNFQK 300  
Db 241 NONYVLKWDYTYANNMTFQVQMLHAFKRNPGNHLKYKQIIPDCENVTTCQVFPQNFQK 300

Db	121	TKDSVMALDGLSFTYSLLIWKNSGVEERIENTYSRHKIYKLSPETTYCLKVKAALLTS	180
Qy	210	WKIGVSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAFLEKRN	269
Db	181	WKIGVSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAFLEKRN	240
Qy	270	PGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQ	329
Db	241	PGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQ	300
Qy	330	AFLPPVFNIRSLSDSFHIIYGAPKQSGNTPVIODYPLIYEIIFWENTNAERKIIIEKKT	389
Db	301	AFLPPVFNIRSLSDSFHIIYGAPKQSGNTPVIODYPLIYEIIFWENTNAERKIIIEKKT	360
Qy	390	DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGN	433
Db	361	DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGN	404

Search completed: January 17, 2006, 07:20:56  
Job time : 33.8172 secs







Matches 212; Conservative 77; Mismatches 137; Indels 10; Gaps 4;

QY 2 MYVLLGATTLVLAVGPWLVSAAGGNLKSPOKVEVDIIDDNFILRNRSDES VGNVTFF 61  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
1 MLAVVGAAALVLVAGAPWLPSAAGGENLKPPENIDVIIDDNYTLKWSSHGSGMGSVTF 60  
QY 62 SPDYQKTGMNDNWLKSGCQNISTKCNBSLKLNVYEEIKLRIRAEKEN-TSSWYVDSPF 120  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
61 SARYRTKDBAKWLKVPEDQHITTKCFSLDNTNVIKTRVRABEGNSTSSWNNEVDPF 120  
QY 121 TPRKAQIGPPEVHLBAEKDAIVIHISPGTKDSVMWALDGLSFTSYLLWKNSSGVEERI 180  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
121 IPTYAHMSPEVRLERADKAILVHISPPQODGNWMALEKPSFSYIRIWOKSSDKKTI 180  
QY 181 ENIYSRHKKYKUSPETTYCLKVKAALLTSWKIVGVSPVHCIKTTVENELPPPNIIEVSQ 240  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
181 NSTYYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSVQCISTTANVKMPVPGNLQVDAQ 240  
QY 241 NQNYVLKWDY-TYANWTFOQWHLAFKRNPNGHLYKKWKOIPDCENVKTTQCVFPQNVFQ 299  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
241 GKSIVLKWDYIAGADVLFRAQWLPFGYSKSSGSHSKDWKEIPTCANVTHCVFSQDTVY 300  
QY 300 KGIYLLRVOASDGNNTSFWSSEIKFKFTEIOAQFLPLPVFNIRISLSDFSFIHYIGAPKSGNT 359  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
301 TGTFEFLHVQAEGNHSTFSNSEKFIDSQKHILPPPPIVTVTAMSDTLVVVNCQDSTCD- 359  
QY 360 PVIQDPYLIYEIIIFWENTSNAEKIIEKTDVTPNLKPLTVYCVARAHTMDKLNKSS 419  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
360 ---GLAYEIIIFWENTSNTKISMEXDGPEFTLKNQLPLTVYCVQARV-LFRALLNKTS 412  
QY 420 VRSDAVCEKTKPGNTS 435  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
413 NFSEKUCEKTRPGSFS 428

RESULT 4  
A47003  
Cytokine receptor family class II protein CRF2-4 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: A47003; G01418  
R;Lutfalla, G.; Gardiner, K.; Uze, G.  
Genomics 16, 366-373, 1993  
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at lesl  
A;Reference number: A47003; MUID:93300510; PMID:8314576  
A;Accession: A47003  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-325 <LU2>  
A;Cross-references: UNIPROT:Q08334; UNIPARC:UPI0000048F14; GB:Z17227; NID:g393378; PID:m  
R;Lutfalla, G.  
submitted to the EMBL Data Library, April 1994  
A;Reference number: G06935  
A;Accession: G01418  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-123, 'D', 125-268, 'VGRME' <LU2>  
A;Cross-references: UNIPARC:UPI00001GA09D; EMBL:U08988; NID:g571295; PID:g571296  
C;Genetics:  
A;Gene: GDB:CRFB4; CRF2-4  
A;Cross-references: GDB:138168; OMIM:123889  
A;Map position: 21q; 21q22.1-21q22.2  
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1  
C;Keywords: transmembrane protein

Query Match 9.9%; Score 228.5; DB 2; Length 325;  
Best Local Similarity 29.9%; Pred. No. 1.3e-09;  
Matches 67; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 19 -WVLSAAGGNLKS-----PKQVEVDIIDDNFILRNRSDES VGNVTFFDYQKTGMD 71  
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
3 WLSGWTGGCILVSAAGVNPVNRNVNFKILQWESPAFAKGNLTFAQY----LS 58

QY 72 NWIKLSCGQNIITSTKCNFSSKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFKKAQIGP 130  
 DB 59 YRIFODKCMNTTITTECDFFS--LSKYGDHITLRVRAEFADSHSDWVNI--TFCPVDDTTIIGP 115  
 QY 131 PEVHLEA-EDKAIVIHISPTKDSV-MWALDGL--SFTYSLLIWNKSSGVVEERIENIYSR 186  
 DB 116 PGHVEVLADSLHMRFLAPKIENEYETWTMKVNVNSWTVNVQVWNGTDEKFIQTTPQYDF 175  
 QY 187 HKIYKLSPEPTYCLKVKAAALLTSWKIGVYSPVHCITKTTVNEELP 230  
 DB 176 EVLRNLEPWTTCVQVRGFLPDRNKAGENSEPCEQTTHDETVP 219

RESULT 5  
 JC6311  
 Interferon receptor-class II cytokine receptor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C/Accession: JC6311  
 R/Gibbs, V.C.; Pennica, D.  
 Gene 186, 97-101, 1997  
 A/Title: CRF2.4: Isolation of cDNA clones encoding the human and mouse proteins.  
 A/Reference number: JC6311; MUID: 97199375; PMID: 9047351  
 A/Accession: JC6311  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-349 <GIB>  
 A/Cross-references: UNIPROT: Q8VHM7; UNIPARC: UPI000017C6DE; GB: U53696

Query Match 9.6%; Score 221.5; DB 2; Length 349;  
 Best Local Similarity 28.1%; Pred. No. 4.9e-09;  
 Matches 64; Conservative 49; Mismatches 86; Indels 29; Gaps 10;

QY 16 VGPWLVLSAAGGKNLKSPOKVEVDIIDNFIILRWNRSDSGVNTFSFDYQ--KTGMNDW 73  
 DB 9 LGGELLVPALG--WIPPEKVRNVSNFNKILQWEVPAPFKTNLTFTAQYESYRSFQDH- 65  
 QY 74 IKLSGQCNITSTKCNFSSKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFKKAQIGPPE 132  
 DB 66 ----CKRTASTQCDFS--HLSKYGDYTVRAELADEHSEWVNV-TFCPVEDTIIGPPE 117  
 QY 133 VHLAEADKAIVIHIS-----PGTKDSVNWALDGL--SFTYSLLIWNKSSGVVEERIENI 183  
 DB 118 MQTESLAESIELRFSAPQIENEPET-----WTLKNYDSWAYRVQYWKNGTNEKFKQVWSP 172  
 QY 184 YSRHKYKLSPEPTYCLKVKAAALLTSWKIGVYSPVHCITKTTVNEELPP 231  
 DB 173 YDSEVRNLNLPWTTCYIQVGFLDQNRKTGEWSEPIC-ERTGNDEITP 219

RESULT 6  
 A49947  
 Interferon gamma receptor beta subunit - mouse  
 N/Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C/Accession: A49947  
 R/Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.  
 Cell 76, 803-810, 1994  
 A/Title: A novel member of the interferon receptor family complements functional  
 A/Reference number: A49947; MUID: 94170381; PMID: 8124717  
 A/Accession: A49947  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-332 <HEM>  
 A/Cross-references: UNIPROT: Q63953; UNIPARC: UPI0000022068; GB: S69336; NID: g5455  
 A/Experimental source: early B-cell line Y16  
 A/Note: sequence extracted from NCBI backbone (NCBIN: 145654, NCBIPI: 145656)  
 C/Keywords: cytokine receptor

Query Match 8.8%; Score 203; DB 2; Length 332;  
 Best Local Similarity 30.1%; Pred. No. 1.1e-07;  
 Matches 69; Conservative 38; Mismatches 86; Indels 36; Gaps 13;

[illegible]

Query Match	8.8%;	Score 203;	DB 2;	Length 332;
Best Local Similarity	30.1%;	Pred. No. 1.1e-07;		
Matches	69;	Conservative	38;	Mismatches 86;
				Indels 36;
				Gaps 13;



[illegible]

[illegible][illegible]

A;Reference number: A31555; MUID:89003065; PMID:2971451

A;Accession: A31555

A;Molecule type: mRNA

A;Residues: 1-489 <AGU>

A;Cross-references: UNIPROT:P15260; UNIPARC:UPI000002CE40; GB:J03143; NID:G184650; PIDN:

C;Genetics:

A;Gene: GDB:IFNGR1; IFNGR

A;Cross-references: GDB:I20688; OMIM:107470

A;Map position: 6q23-6q24

C;Superfamily: interferon gamma receptor

C;Keywords: cytokine receptor; transmembrane protein

Query Match 5.1%; Score 118; DB 2; Length 489;

Best Local Similarity 22.2%; Pred. No. 0.42;

Matches 50; Conservative 39; Mismatches 102; Indels 34; Gaps 10;

Qy 227 NELPPENIEVSQNVQNVKWDYTYANM--TFQVOMLHAPLKNPGNHLKWKQIPDCE 284

Db 27 SSVPTPTNVTTIESYNNMPIVTWEYQIIMPQVPVFTVE-----VKYGVKSEW--IDACI 78

Qy 285 NVKTKTCVFPQNVFQKGIYL-LRYQASDGNNTSFWSEBEIKFDTETIOAFLPPPVFNIRS-- 341

Db 79 NISHHYCNI SDHVGDPNSLWVRVKARVGQKESAYAKSEFAVCRDGIKGPPLDIRKEE 138

Qy 342 ----LSDSFH--IYIGAPKQSGN-TPVIQDYPLIYIIFWNTSNAERKILIEKKTQD----- 390

Db 139 KQIMIDIFHPSVFGVDEYDYPETTCYIRVNVVVRMNGSEIQYKILTQKEDDCDEI 198

Qy 391 ---VTVPNLKLPLTVYCVKARA--HTMDEKLNKS-----SVFSDAV 425

Db 199 QCQLAIPVSLNSQYCVSAEGVLHWGVTEKSEKVCITIPNSSI 243

#### RESULT 15

S51604

receptor-like tyrosine kinase Etk-1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 29-May-1998

C;Accession: S51604

R;Maisonpierre, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam

A;Reference number: S49015; MUID:9406777; PMID:7504232

A;Accession: S51604

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-981 <MAI>

A;Cross-references: UNIPARC:UPI0000175666; EMBL:S68029

A;Note: the authors translated the codon GAC for residue 170 as Glu

C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C;Keywords: Atp; transmembrane protein

F;651-917/Domain: protein kinase homology <KIN>

F;659-667/Region: protein kinase Atp-binding motif

Query Match 5.1%; Score 118; DB 2; Length 981;

Best Local Similarity 20.1%; Pred. No. 1.1;

Matches 92; Conservative 51; Mismatches 165; Indels 150; Gaps 21;

Qy 27 GKNLKSPQKVEVDII--DDNF-----ILRWNRSDSESGVNT---PSFDYQKTKGMDNW 73

Db 165 GRNIKDNQYIKIDITAADESFTLDELDRVMKLNTEVRDVGFLSKKGFYLAQDVG----- 220

Qy 74 IKLSGCQNITST-----KCNFSSLKLVYVEIKLIRAEKENTSSWYEVDSFTPRKQAI 128

Db 221 ----ACTALVSVRVYKCPSPVRHLAVFPD-----TITGADSSQLLEVSQSVNHSVTD 271

Qy 129 GPPEVHLEAEKAVIHIISPTGKDSVMWALDGLSFTYSLIWKNSSGVVEERIENI-YSRH 187

Db 272 DPKKHCASGEWLV-----PIGKMC-----KAGYEKNKGTQCVCRP 309

Qy 188 KIYKLSPETTYCLKYKAAALLTSWKIGVYSPVH-----CIKTTVNELEPP----- 231

Db 310 GFFKASPHSQTCSCPP-----HSYTHEASTSCVCEKDYFRFESDPTTMACTRP 359

Qy 232 ----PENIEVSQNVQNVVLK-----DYTYANMTFOVOMLHAPLKNPGNHLKWK 278

Db 360 PSAPRNAISNVNETSVFLEWIPPADTGGGRDVSYYILCKCN-SHAGVCECGGHR-- 415

Qy 279 QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEBEIKFDTETIOAFLPPPVFN 338

Db 416 -----YLPQQIGLKNTSVMMADPLAHTNYTF-----EIEA-----VNG 448

Qy 339 IRSLSDSFHIYIG---APKQSGNTPVIQ-----DYP-----LIYEIF 373

Db 449 VSDLSPTGTRYVSVNVVTNQAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY 508

Qy 374 WENTSNAERKILIE-KKTDVTVPNLKLPLTVYCVKARAHT 410

Db 509 FEKQDQETSYTIISKETTITAEGLKPASVYVFOIRART 546

Search completed: January 17, 2006, 07:19:42

Job time : 27.5245 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 07:18:53 ; Search time 88.5544 Seconds  
(without alignments)  
2057.195 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MNVLLGATTLVLVAGPWV.....KSSVFSDAVCEKTPGNTSK 436

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2313	100.0	436	3	US-09-240-675-2
2	2313	100.0	436	4	US-10-824-981-2
3	2313	100.0	436	5	US-10-473-127-1756
4	2313	100.0	436	5	US-10-473-127-1758
5	2313	100.0	436	5	US-10-473-127-1764
6	2313	100.0	557	3	US-09-240-675-4
7	2313	100.0	557	4	US-10-358-228-3
8	2313	100.0	557	5	US-10-473-127-1757
9	2313	100.0	557	5	US-10-473-127-1759
10	2313	100.0	557	5	US-10-473-127-1760
11	2313	100.0	557	5	US-10-473-127-1763
12	2313	100.0	557	5	US-10-473-127-1765
13	2313	100.0	557	5	US-10-473-127-1766
14	2313	100.0	557	5	US-10-473-127-1772
15	2313	100.0	557	5	US-10-473-127-1773
16	2309	99.8	557	5	US-10-473-127-1768
17	2308	99.8	557	4	US-10-824-981-4
18	2308	99.8	557	5	US-10-473-127-1769
19	2307	99.7	557	5	US-10-473-127-1761
20	2304	99.6	436	5	US-10-473-127-1767
21	2302	99.5	575	3	US-09-925-300-1672
22	2302	99.5	575	5	US-10-473-127-1762
23	2287	98.9	575	5	US-10-450-763-47653
24	2279	98.5	441	5	US-10-764-833-41
25	2260	97.7	434	5	US-10-473-127-1770
26	2208	95.5	496	5	US-10-473-127-1771
27	1507	65.2	560	4	US-10-293-832-29

28 1500 64.9 560 4 US-10-293-832-30 Sequence 30, Appl  
29 510.5 22.1 198 4 US-10-293-832-33 Sequence 33, Appl  
30 236.5 10.2 273 4 US-10-186-180-15 Sequence 15, Appl  
31 234.5 10.1 273 4 US-10-186-180-14 Sequence 14, Appl  
32 233.5 10.1 220 3 US-09-925-055D-19 Sequence 19, Appl  
33 233.5 10.1 220 4 US-10-807-837-44 Sequence 44, Appl  
34 233.5 10.1 273 4 US-10-186-180-2 Sequence 2, Appl  
35 233.5 10.1 273 4 US-10-358-228-8 Sequence 8, Appl  
36 233.5 10.1 476 3 US-09-925-055D-23 Sequence 23, Appl  
37 233.5 10.1 476 4 US-10-104-919-62 Sequence 62, Appl  
38 233.5 10.1 476 4 US-10-395-741B-63 Sequence 63, Appl  
39 233.5 10.1 476 5 US-10-968-432-62 Sequence 62, Appl  
40 232.5 10.1 273 4 US-10-186-180-16 Sequence 16, Appl  
41 228.5 9.9 325 3 US-09-870-574-3 Sequence 3, Appl  
42 228.5 9.9 325 3 US-09-949-192-5 Sequence 5, Appl  
43 228.5 9.9 325 4 US-10-052-586-390 Sequence 390, App  
44 228.5 9.9 325 4 US-10-066-500-137 Sequence 137, App  
45 228.5 9.9 325 4 US-10-174-590-390 Sequence 390, App

## ALIGNMENTS

RESULT 1  
US-09-240-675-2  
; Sequence 2, Application US/09240675  
; Patent No. US20020055492A1  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240.675  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/307.588  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 436 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-240-675-2

Query Match 100.0%; Score 2313; DB 3; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120

Qy 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
Db 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPEPTYCLKVAALITTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLKVAALITTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240

Qy 241 NONVLLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVLLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAPLLPPVFNIRSLSDSFPHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAPLLPPVFNIRSLSDSFPHIYIGAPKQSGNTP 360

Qy 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 2  
US-10-824-981-2  
; Sequence 2, Application US/10824981  
; Publication No. US20040191840A1  
; GENERAL INFORMATION:  
; APPLICANT: Benoît, Patrick  
; APPLICANT: Maguire, Deborah  
; APPLICANT: Plavec, Ivan  
; APPLICANT: Tovy, Michael  
; APPLICANT: Meyer, Francois  
; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With  
; FILE REFERENCE: A-72230-2  
; CURRENT APPLICATION NUMBER: US/10/824,981  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US 09/240,675  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: US 08/307,588  
; PRIOR FILING DATE: 1994-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP93/00770  
; PRIOR FILING DATE: 1993-03-30  
; PRIOR APPLICATION NUMBER: EP 92400902.0  
; PRIOR FILING DATE: 1992-03-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-824-981-2

Query Match 100.0%; Score 2313; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120

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Db 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180

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Db 241 NONVLLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

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Db 301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAPLLPPVFNIRSLSDSFPHIYIGAPKQSGNTP 360

Qy 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 3  
US-10-473-127-1756  
; Sequence 1756, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1756  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1756

Query Match 100.0%; Score 2313; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKQVEVDIIDDNFILRNRSDESNGVT 60

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Qy 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTPGNTSK 436  
Db 421 FSDAVCEKTPGNTSK 436

## RESULT 4

US-10-473-127-1758  
; Sequence 1758, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1758  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1758

Query Match 100.0%; Score 2313; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLLVAVGPWVLSAAGGKNLSPQKVEVDIIDDNFILRNRSDSVGNVT 60  
Db 1 MMVLLGATTLLVAVGPWVLSAAGGKNLSPQKVEVDIIDDNFILRNRSDSVGNVT 60  
Qy 61 FSDYQKTGMDNWKLSGQNIITSTKCNFSSILKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMDNWKLSGQNIITSTKCNFSSILKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180

Qy 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRQVQSGNNTSFSEBEIKFDTETQAFLLPVPFNIRSLSDSFHYIYGAPKOSGNT 360  
Db 301 GIYLLRQVQSGNNTSFSEBEIKFDTETQAFLLPVPFNIRSLSDSFHYIYGAPKOSGNT 360  
Qy 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTPGNTSK 436  
Db 421 FSDAVCEKTPGNTSK 436

## RESULT 5

US-10-473-127-1764  
; Sequence 1764, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1764  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1764

Query Match 100.0%; Score 2313; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLLVAVGPWVLSAAGGKNLSPQKVEVDIIDDNFILRNRSDSVGNVT 60  
Db 1 MMVLLGATTLLVAVGPWVLSAAGGKNLSPQKVEVDIIDDNFILRNRSDSVGNVT 60  
Qy 61 FSDYQKTGMDNWKLSGQNIITSTKCNFSSILKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMDNWKLSGQNIITSTKCNFSSILKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300

Db 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPVPFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPVPFNIRSLSDSFHYIYGAPKQSGNTP 360  
Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 6  
US-09-240-675-4  
; Sequence 4, Application US/09240675  
; Patent No. US20020055492A1  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: FLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA: US/09/240,675  
; APPLICATION NUMBER: US/09/240,675  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; APPLICATION NUMBER: PCI/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-240-675-4

Query Match 100.0%; Score 2313; DB 3; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNRSDESUGNVT 60  
Db 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNRSDESUGNVT 60

Qy 61 FSPDYQKTGMNDWIKLSGCCQNTITSTKCNFSSSLKLVNVEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSGCCQNTITSTKCNFSSSLKLVNVEEIKLIRAEKENTSSWYEVDSF 120

Qy 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240

Qy 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPVPFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPVPFNIRSLSDSFHYIYGAPKQSGNTP 360

Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 7  
US-10-358-228-3  
; Sequence 3, Application US/10358228  
; Publication No. US20030211578A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: Interferon Receptor HKAEF92  
; FILE REFERENCE: PF465C1  
; CURRENT APPLICATION NUMBER: US/10/358,228  
; CURRENT FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: 09/453,569  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: 09/326,216  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 60/088,185  
; PRIOR FILING DATE: 1998-06-05  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-358-228-3

Query Match 100.0%; Score 2313; DB 4; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNRSDESUGNVT 60  
Db 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNRSDESUGNVT 60

Qy 61 FSPDYQKTGMNDWIKLSGCCQNTITSTKCNFSSSLKLVNVEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSGCCQNTITSTKCNFSSSLKLVNVEEIKLIRAEKENTSSWYEVDSF 120

Qy 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240

QY 241 NONTYLVKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONTYLVKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
QY 421 PSDAVCEKTKPGNTSK 436  
DB 421 PSDAVCEKTKPGNTSK 436

## RESULT 8

US-10-473-127-1757  
; Sequence 1757, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1757  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1757

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGPNWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVDGNT 60  
DB 1 MMVLLGATTLLVAVGPNWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVDGNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
DB 121 TPFRKAQIGPPVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
QY 241 NONTYLVKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONTYLVKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420

DB 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
QY 421 PSDAVCEKTKPGNTSK 436  
DB 421 PSDAVCEKTKPGNTSK 436

## RESULT 9

US-10-473-127-1759  
; Sequence 1759, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1759  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1759

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGPNWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVDGNT 60  
DB 1 MMVLLGATTLLVAVGPNWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVDGNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
DB 121 TPFRKAQIGPPVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
QY 241 NONTYLVKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONTYLVKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 10  
US-10-473-127-1760  
; Sequence 1760, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1760  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1760

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60  
Qy 61 FSPDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSPDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Qy 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFYSLLIWKNSSGVEERI 180  
Db 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFYSLLIWKNSSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPEYTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEYTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Qy 241 NONVVLKWDVTYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NONVVLKWDVTYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFOK 300  
Qy 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360  
Db 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360  
Qy 361 VIQDYPLIYIIIFWNTSNAERKIIIEKTDVTPVNLKPLTVYCVKAAHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYIIIFWNTSNAERKIIIEKTDVTPVNLKPLTVYCVKAAHTMDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 12  
US-10-473-127-1765  
; Sequence 1765, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.

RESULT 11  
US-10-473-127-1763  
; Sequence 1763, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1763  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1763

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60  
Qy 61 FSPDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSPDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Qy 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFYSLLIWKNSSGVEERI 180  
Db 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFYSLLIWKNSSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPEYTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEYTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Qy 241 NONVVLKWDVTYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NONVVLKWDVTYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFOK 300  
Qy 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360  
Db 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360  
Qy 361 VIQDYPLIYIIIFWNTSNAERKIIIEKTDVTPVNLKPLTVYCVKAAHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYIIIFWNTSNAERKIIIEKTDVTPVNLKPLTVYCVKAAHTMDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1765  
; LENGTH: 557  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-473-127-1765

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGPNVLSAAAGGKNLSPQKVEVDIIDDNFILRNRSDESVGNT 60  
DB 1 MMVLLGATTLLVAVGPNVLSAAAGGKNLSPQKVEVDIIDDNFILRNRSDESVGNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGSGVERI 180  
DB 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGSGVERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
QY 241 NONVYLKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONVYLKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIQAFLLPPVFNIRSLDSFSFHIYIGAPKSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIQAFLLPPVFNIRSLDSFSFHIYIGAPKSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 13  
US-10-473-127-1766  
; Sequence 1766, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1766  
; LENGTH: 557  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-473-127-1766

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGPNVLSAAAGGKNLSPQKVEVDIIDDNFILRNRSDESVGNT 60  
DB 1 MMVLLGATTLLVAVGPNVLSAAAGGKNLSPQKVEVDIIDDNFILRNRSDESVGNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGSGVERI 180  
DB 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGSGVERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
QY 241 NONVYLKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONVYLKWDYTYANNMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIQAFLLPPVFNIRSLDSFSFHIYIGAPKSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIQAFLLPPVFNIRSLDSFSFHIYIGAPKSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 14  
US-10-473-127-1772  
; Sequence 1772, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01



; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1772  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1772

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVLLGATTLLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
Db 1 MMVLLGATTLLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
  
Qy 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
  
Qy 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
Db 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
  
Qy 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
  
Qy 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCFFQNVFOK 300  
Db 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCFFQNVFOK 300  
  
Qy 301 GIYLLRVQASDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
  
Qy 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 15

US-10-473-127-1773  
; Sequence 1773, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1773  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1773

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVLLGATTLLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
Db 1 MMVLLGATTLLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
  
Qy 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
  
Qy 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
Db 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
  
Qy 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
  
Qy 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCFFQNVFOK 300  
Db 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCFFQNVFOK 300  
  
Qy 301 GIYLLRVQASDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
  
Qy 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

Search completed: January 17, 2006, 07:35:29  
Job time : 89.5544 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:19:53 ; Search time 17.7109 Seconds  
(without alignments)  
232.741 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVLLGATLVLVAVGPWV.....KSSVFSFVAVCKTKPGNTSK 436

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA New:\*
- 1: /cgn2\_6/prodata/2/pubpaa/US08 NEW PUB.pbp.\*
  - 2: /cgn2\_6/prodata/2/pubpaa/US06 NEW PUB.pbp.\*
  - 3: /cgn2\_6/prodata/2/pubpaa/US07 NEW PUB.pbp.\*
  - 4: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pbp.\*
  - 5: /cgn2\_6/prodata/2/pubpaa/US09 NEW PUB.pbp.\*
  - 6: /cgn2\_6/prodata/2/pubpaa/US10 NEW PUB.pbp.\*
  - 7: /cgn2\_6/prodata/2/pubpaa/US11 NEW PUB.pbp.\*
  - 8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200	8.6	542	6	US-10-131-826A-188
2	198	8.6	553	6	US-10-636-716-2
3	198	8.6	553	6	US-10-636-716-14
4	198	8.6	553	6	US-10-636-716-16
5	198	8.6	553	6	US-10-636-716-18
6	198	8.6	553	6	US-10-636-716-20
7	198	8.6	553	6	US-10-636-716-22
8	198	8.6	553	6	US-10-636-716-24
9	198	8.6	553	6	US-10-636-716-26
10	198	8.6	553	6	US-10-636-716-28
11	198	8.6	553	6	US-10-636-716-30
12	198	8.6	553	6	US-10-636-716-32
13	198	8.6	553	6	US-10-636-716-34
14	198	8.6	553	6	US-10-636-716-36
15	198	8.6	553	6	US-10-636-716-38
16	198	8.6	553	6	US-10-636-716-40
17	198	8.6	553	6	US-10-636-716-42
18	198	8.6	553	6	US-10-636-716-44
19	198	8.6	553	6	US-10-636-716-46
20	198	8.6	553	6	US-10-636-716-48
21	174.5	7.5	221	6	US-10-636-716-56
22	169.5	7.3	221	6	US-10-636-716-54
23	168.5	7.3	221	6	US-10-636-716-50
24	168.5	7.3	384	7	US-11-075-351-12
25	168.5	7.3	404	7	US-11-075-351-23

26	168.5	7.3	404	7	US-11-075-351-25
27	167.5	7.2	221	6	US-10-636-716-52
28	165.5	7.2	221	6	US-10-636-716-60
29	162.5	7.0	221	6	US-10-636-716-58
30	151.5	6.5	366	7	US-11-075-351-38
31	151	6.5	574	7	US-11-102-240-164
32	149.5	6.5	374	7	US-11-075-351-42
33	147.5	6.4	311	6	US-10-131-826A-32
34	147.5	6.4	311	6	US-10-512-214-16
35	123	5.3	522	7	US-11-184-399-8
36	118	5.1	1005	7	US-11-113-424-63
37	117.5	5.1	2214	7	US-11-080-991-94
38	115	5.0	244	7	US-11-184-399-10
39	115	5.0	473	7	US-11-165-141-23
40	115	5.0	520	7	US-11-098-662-12
41	115	5.0	520	7	US-11-165-141-19
42	115	5.0	599	7	US-11-165-141-33
43	109	4.7	203	7	US-11-165-141-4
44	109	4.7	491	7	US-11-098-662-14
45	109	4.7	491	7	US-11-165-141-2

ALIGNMENTS

RESULT 1  
US-10-131-826A-188  
; Sequence 188, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.

```

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 188
; LENGTH: 542
; TYPE: PR
; ORGANISM: Homo Sapien
US-10-131-826A-188

Query Match
Best Local Similarity 8.6%; Score 200; DB 6; Length 542;
Matches 91; Conservative 80; Mismatches 172; Indels 90; Gaps 17;

QY 11 LVLVAGPW--VLSAAGGNLSPKQVEVDIIDNPFILNRNDSVGV-NVTFSFDYQK 67
Db 7 LLLLAAPWGRAVPCVSG--LPKPANITFLSINNMKNVLQWTPPEGLQGVKVTYVQYFI 64

QY 68 TGMONWIKLSCQNTITKCNFSLKLVYEEIKLRIRA-EKENTSSWYEVDSFTPRKA 126
Db 65 YGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVAIWTGKCSKWAESGRFPFLET 124

QY 127 QIGPPEVHLEADKAIVHISPGTK-----DSVMALDGLSFTYSLLIWNKSSGVE 177
Db 125 QIGPPEVALTTDEKISVVLTAPEKWKRNEDLPVSMQIYSLNLYNVSVLNKSRTWS 184

QY 178 ERIENIYSHKIYK--LSPETTYCLKVAALLTSWKIGVYSPVHCITVTENE----- 228
Db 185 QCVTN-----HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCAKTLKQDSSEFKAKI 240

QY 229 -----LPPENIEVSQNVQNYVLKWDYTYANMTFOV-QWLHAFKRNPGNHLKWKQIPD 282
Db 241 IFWVLP-----ISITV-----FLFSVMGYSIYRIHVGEKHPANLI----- 278

QY 283 CENVKTTQCVFPQNVFQKGYLLRVQASDGNNTSFWSEEEKFDTETI---QAFLLPPVFNI 339
Db 279 -----LIYGNFDRKFFV-----PAEKIVINFITLINSDDSKI SHQDMSLLGKSSDV 325

QY 340 RLSLDSFHIYIGAPKQSGNTVPVIQDYPLIYEI-----IFWENTSNAERKIEKKTVD 391
Db 326 SSLND-----PQPSGNLRPPQBEVEVKHGLVASHLMEIFCDSEBNTGTSFTQOESL 377

QY 392 --TVPNLKPLTVY 402
Db 378 SRTIPDPKTVIEY 390

RESULT 2
US-10-636-716-2
; Sequence 2, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-2

Query Match
Best Local Similarity 8.6%; Score 198; DB 6; Length 553;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAGPW--VLSAAGGNLSPKQVEVDIIDNPFILNRNDSVGV-NVTFSFDYQK 67
Db 18 LLLLAAPWGRAVPCVSG--LPKPANITFLSINNMKNVLQWTPPEGLQGVKVTYVQYFI 75

QY 68 TGMONWIKLSCQNTITKCNFSLKLVYEEIKLRIRA-EKENTSSWYEVDSFTPRKA 126
Db 76 YGQKWLKNSCRNINRTYCDLSAETSDYEHQYAKVAIWTGKCSKWAESGRFPFLET 135

QY 127 QIGPPEVHLEADKAIVHISPGTK-----DSVMALDGLSFTYSLLIWNKSSGVE 177
Db 136 QIGPPEVALTTDEKISVVLTAPEKWKRNEDLPVSMQIYSLNLYNVSVLNKSRTWS 195

QY 178 ERIENIYSHKIYK--LSPETTYCLKVAALLTSWKIGVYSPVHCITVTENE----- 228
Db 196 QCVTN-----HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCAKTLKQDSSEFKAKI 251

QY 229 -----LPPENIEVSQNVQNYVLKWDYTYANMTFOV-QWLHAFKRNPGNHLKWKQIPD 282
Db 252 IFWVLP-----ISITV-----FLFSVMGYSIYRIHVGEKHPANLI----- 289

QY 283 CENVKTTQCVFPQNVFQKGYLLRVQASDGNNTSFWSEEEKFDTETI---QAFLLPPVFNI 339
Db 290 -----LIYGNFDRKFFV-----PAEKIVINFITLINSDDSKI SHQDMSLLGKSSDV 336

QY 340 RLSLDSFHIYIGAPKQSGNTVPVIQDYPLIYEI-----IFWENTSNAERKIEKKTVD 391
Db 337 SSLND-----PQPSGNLRPPQBEVEVKHGLVASHLMEIFCDSEBNTGTSFTQOESL 388

QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 3
US-10-636-716-14
; Sequence 14, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.

```

TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA.  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-14

Query Match 8.6%; Score 198; DB 6; Length 553;  
Best Local Similarity 21.0%; Pred. No. 1.1e-09;  
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;  
QY 11 LVLVAVGPW--VLSAAGGKNLSPQKVEVDIIDNFILRNWRSDESVG-NVTFSFDYQK 67  
DB 18 LLLLLAAPGRAWPCVSGG--LPKANITFLSINMKVNLQWTPPEGLQGVKVTYTVQYFI 75  
QY 68 TGMNDWIKLSCGNITSTKCNFSSLLKNVVEIKLPIRA-EKENTSSWYEVDSFTPRKA 126  
DB 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKCSKWAESGRFPFLET 135  
QY 127 QIGPPEVHLEADKAIVHISPGTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177  
DB 136 QIGPPEVALTTDEKISVLTAPKWKRPEDLPVSMQIYSLNKNVSVLNTKSNRTWS 195  
QY 178 ERIENTYSRHKIYK--LSPETTYCLVKAALTSWKIGYVSPVHCITKTIVENE----- 228  
DB 196 QCVTN---HTVLVLTWLEPTLYCVHVESFVPQPPRRAQPSKQCARTLKQDSSEPKAKI 251  
QY 229 -----LPPNTEVSVQNYVNLKWDYTYANMTFQV-QWLHAFKRNPGNHLKWKQIPD 282  
DB 252 IFWYVLP-----ISITY-----FLFSVMGYSIYRYIHVGKEXHPANLI----- 289  
QY 283 CENVKTTQCVFQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDEI---QAFLLPVENI 339  
DB 290 -----LIVGNEFDKRFV-----PAEKIVINFITLMSDDSKHSDMSLLGKSSDV 336  
QY 340 RSLSDSFHVIYIGAPKQSGNTPVIQDYPLIYEI-----IFWNTSNAERKIIIEKKTVD 391

DB 337 SSLND-----POPSGNLRPPQBEVEVKHILGYASHLMWEIFCDSEENTEGTFTQOESL 388  
QY 392 --TVPNLKLPLTVY 402  
DB 389 SRTIPDPKTVIEY 401  
RESULT 4  
US-10-636-716-16  
Sequence 16, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelnberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrish, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc. East  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-16

Query Match 8.6%; Score 198; DB 6; Length 553;  
Best Local Similarity 21.0%; Pred. No. 1.1e-09;  
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;  
QY 11 LVLVAVGPW--VLSAAGGKNLSPQKVEVDIIDNFILRNWRSDESVG-NVTFSFDYQK 67  
DB 18 LLLLLAAPGRAWPCVSGG--LPKANITFLSINMKVNLQWTPPEGLQGVKVTYTVQYFI 75  
QY 68 TGMNDWIKLSCGNITSTKCNFSSLLKNVVEIKLPIRA-EKENTSSWYEVDSFTPRKA 126  
DB 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKCSKWAESGRFPFLET 135



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; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-20

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGKLNKSPQKVEVDIIDNFILRNWRSDESVG-NVTFSDYQK 67
DB 18 LLLLLAAPGRAWPCVSGG--LPKPANITFLSNKQVLTQWTPPEGLQGVKVTYTVQYFI 75
QY 68 TGMNDWIKLGGCONITSTKCNFSSKLNVYEEKLRIRA-EKENTSSWYEVDSFTPRKA 126
DB 76 YQKKWLKNSKCRNIRTYCDLSAETSDYEHQYAKVKAIWGTCCKWAESGRFYPFLET 135
QY 127 QIGPPEVHLAEADKAIVIHISGTK-----DSVMWALDGLSFTYSLLIWKNSSGVE 177
DB 136 QIGPPEVALTTDEKISVVLTAPEKWKRNPELPSVMOQIYSNLKYNVSLNKTNSRTWS 195
QY 178 ERIENIYSHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE----- 228
DB 196 QCVTN-----HTLVLTWLENTLYCVHVESFVPGPPRAQPSKQKARTLKQSSSEPKAKI 251
QY 229 -----LPPPENIEVSQNVQNYVLKWDYTYANMTFOV--OHLHAFLEKRNPGNHLKWKQIPD 282
DB 252 IFWYVLP-----ISITV-----FLFSVMGYSIVRYIHVGKEXHPANLI----- 289
QY 283 CENVKTTQCVPFQNVFQKGIYLLRVOASDGNNTSFWSBEIKFDTETI---OAFLLPPVFN 339
DB 290 -----LIYGNEDFKRFV---PAEKIVINFITLNSDDSKISHQDMSLLGKSSDV 336
QY 340 RLSLDSFHIYIGAPKQSGNTPVQIDYPLIYEI-----IFWENTSNAERKIEKKTVD 391
DB 337 SSLND-----POPSGNLRPPQEEBVKHLYASHLMEIFCDSEBTEGTSFTQOESL 388
QY 392 --TVPNLKPLTVY 402
DB 389 SRTIPDPKTVIEY 401

RESULT 7
US-10-636-716-22
; Sequence 22, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
```

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; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-22
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```
Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGKLNKSPQKVEVDIIDNFILRNWRSDESVG-NVTFSDYQK 67
DB 18 LLLLLAAPGRAWPCVSGG--LPKPANITFLSNKQVLTQWTPPEGLQGVKVTYTVQYFI 75
QY 68 TGMNDWIKLGGCONITSTKCNFSSKLNVYEEKLRIRA-EKENTSSWYEVDSFTPRKA 126
DB 76 YQKKWLKNSKCRNIRTYCDLSAETSDYEHQYAKVKAIWGTCCKWAESGRFYPFLET 135
QY 127 QIGPPEVHLAEADKAIVIHISGTK-----DSVMWALDGLSFTYSLLIWKNSSGVE 177
DB 136 QIGPPEVALTTDEKISVVLTAPEKWKRNPELPSVMOQIYSNLKYNVSLNKTNSRTWS 195
QY 178 ERIENIYSHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE----- 228
DB 196 QCVTN-----HTLVLTWLENTLYCVHVESFVPGPPRAQPSKQKARTLKQSSSEPKAKI 251
QY 229 -----LPPPENIEVSQNVQNYVLKWDYTYANMTFOV--OHLHAFLEKRNPGNHLKWKQIPD 282
DB 252 IFWYVLP-----ISITV-----FLFSVMGYSIVRYIHVGKEXHPANLI----- 289
QY 283 CENVKTTQCVPFQNVFQKGIYLLRVOASDGNNTSFWSBEIKFDTETI---OAFLLPPVFN 339
DB 290 -----LIYGNEDFKRFV---PAEKIVINFITLNSDDSKISHQDMSLLGKSSDV 336
QY 340 RLSLDSFHIYIGAPKQSGNTPVQIDYPLIYEI-----IFWENTSNAERKIEKKTVD 391
DB 337 SSLND-----POPSGNLRPPQEEBVKHLYASHLMEIFCDSEBTEGTSFTQOESL 388
```

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QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDKTVIEY 401

RESULT 8
US-10-636-716-24
; Sequence 24, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-24

Query Match 8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGKGLKSPQKVEVDIIDDNFILRNWRSDESUG-VNTPSFYQK 67
Db 18 LLLLLAPWGRAPVCVSGG--LPKPANITFISINKNVQLQMTPEGLQGQGVKVTYVQYFI 75
QY 68 TGMNDWIKLSCQNTITKCNFFSLKLNVEIEIKLRIR-AEKENTSSWYEVDSFTPRKA 126
Db 76 YGQKKWLKNSCRNINRTYCDLSAETSDEYHQYAKVKAIWGTCCKWAESGRYPFLET 135
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177

Db 136 QIGPPEVALTTDEKSIISVLTAPKWKRNKPNEDLPVSMQOIYSNLKYNVSLMTKSNRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLVKVKAALLTSWKIGVYSPVHCITKTVENE----- 228
Db 196 QCVTN-----HTLVLTWLEPNLYCVHVESFVPGPPRAQPSKQKQARTLKQOSSSEFKAKI 251
QY 229 -----LPPPENIEVSQONQNYLVKWDYTYANMTFQV--QWLHAFILKRNFGNHLKWKQIPD 282
Db 252 IFWVVLPL-----ISITV-----FLFSVMGYSIYRYIHVGKEKHPANLI----- 289
QY 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSBEIKFDTEI-----QAPLLPVPVNI 339
Db 290 -----LIYGNFEDKRFV-----PAEKIVINFITLNISSDKISHQDMSLLGKSSDV 336
QY 340 RSLSDSFHIYIGAPKQSCNTPVIODYPLIYEI-----IFWENTSNAERKILIEKKTVDV 391
Db 337 SSLND-----PQPSGNLRPPQEEBEVKGHLGYASHLMEIFCDSEENTEGETSFTQOSSL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDKTVIEY 401

RESULT 9
US-10-636-716-26
; Sequence 26, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```



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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-26

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGNLKSPQKVEVDIIDDNFILRNRSDESVG-NVTFSPDYQK 67
Db 18 LLLLLAAPGWRAPVPCVSGG--LPKPANITFLSINMKNVLTQWTPPEGLQGVKVTYTVQYFI 75
QY 68 TGMNDWIKLGGCONITSTKCNFSSSLKLVYEEIKLIRA-EKENTSSWEVDSFTPRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTCKSKWAESGRFYFPFLET 135
QY 127 QIGPPVHLEADKATVIHISPTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177
Db 136 QIGPPEVALTTDEKSISSVLTAPKWKRNPEDLFVSMQOIYSNLKYNVSVLNTKSNRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLKVKAALITSMKIGVYSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLENTLYCVHVSFVPGPPRAQSEKQCARTLKQSSSEFKAKI 251
QY 229 -----LPPENIEVSQONQYVLKWDYTYANMTFQV-OMLHAFKRNPGNHLKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRVIVHGKXHPANLI----- 289
QY 283 CENVKTTQCVFPQNVQKGIYLLRVQASDGNNTSFWESEIKPDEI---QAFLLPPVFN 339
Db 290 -----LYGNEFDKRFV---PAEKIVINFTILNISDDSKISHQDMSLLGKSDV 336
QY 340 RSLSDSFHIYIGAPKQSGNTPVTDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQSGNLRPQEEVKHGLGYASHLMEIFCDSENTGTSFTQOESL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDKTVIEY 401

RESULT 11
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGNLKSPQKVEVDIIDDNFILRNRSDESVG-NVTFSPDYQK 67
Db 18 LLLLLAAPGWRAPVPCVSGG--LPKPANITFLSINMKNVLTQWTPPEGLQGVKVTYTVQYFI 75
QY 68 TGMNDWIKLGGCONITSTKCNFSSSLKLVYEEIKLIRA-EKENTSSWEVDSFTPRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTCKSKWAESGRFYFPFLET 135
QY 127 QIGPPVHLEADKATVIHISPTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177
Db 136 QIGPPEVALTTDEKSISSVLTAPKWKRNPEDLFVSMQOIYSNLKYNVSVLNTKSNRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLKVKAALITSMKIGVYSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLENTLYCVHVSFVPGPPRAQSEKQCARTLKQSSSEFKAKI 251
QY 229 -----LPPENIEVSQONQYVLKWDYTYANMTFQV-OMLHAFKRNPGNHLKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRVIVHGKXHPANLI----- 289
QY 283 CENVKTTQCVFPQNVQKGIYLLRVQASDGNNTSFWESEIKPDEI---QAFLLPPVFN 339
Db 290 -----LYGNEFDKRFV---PAEKIVINFTILNISDDSKISHQDMSLLGKSDV 336
QY 340 RSLSDSFHIYIGAPKQSGNTPVTDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQSGNLRPQEEVKHGLGYASHLMEIFCDSENTGTSFTQOESL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDKTVIEY 401

RESULT 11
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
```

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
US-10-636-716-30

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGCKNLKSPQKVEVDIIDNFILRNWRSDESVG-VNTPSFEDYQK 67
Db 18 LLLLAAPWGRAVPCVSGG--LPKPANITFLSINNKNVLQMTTPPEGLOGVKVYTYTVQVFI 75
QY 68 TGMNDWIKLSGQNTITSTKCNFSSLLKLVYBEIKLIRA-EKENTSSWVEVDSFPPFKA 126
Db 76 YGQKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCCKWAESGRFYPFLET 135
QY 127 QIGPPEVHLEADKAIVTHISPGTK-----DSVMWALDGLSFTYSLLIWKNSSGVE 177
Db 136 QIGPPEVALTTDEKISVVLTAPEKWRNPEDLPVSMQQLYSNLKYNVSLNLTGKSNRTWS 195
QY 178 ERIENIYSHKIYK--LSPETTYCLKVAALTSWKIGVYSPVHCITVENE----- 228
Db 196 QCVTN-----HTLVLTWLEPTLYCVHVSFVPGPPRAQPSKQKARTLKQSSBFKAKI 251
QY 229 -----LPPPENIEVSQONQYVLKWDYTYANNTFQV-OWLHAFKLRNPNHLYKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLPSVMGYSIYRIYHVHGEKHPANLI----- 289
QY 283 CENVKTCQVPQNFQKGIYLLRVOASDGNNTSPWSEIEKPDTEI---QAPLLPPVFN 339
Db 290 -----LIYGNEDKRFV---PAEKIVINFTILNISDSKISHQDMSLLGKSDV 336
QY 340 RSLSDSFHYIYGAPQSGNTVPIDYPLIYEI-----IFWENTSNAERKIEKKTVDV 391
Db 337 SSLND-----POPSGNLRNPQBEIEVKHGLGYASHLMEIFCDSEENTGTSFTQBSL 388

CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
US-10-636-716-30

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGCKNLKSPQKVEVDIIDNFILRNWRSDESVG-VNTPSFEDYQK 67
Db 18 LLLLAAPWGRAVPCVSGG--LPKPANITFLSINNKNVLQMTTPPEGLOGVKVYTYTVQVFI 75
QY 68 TGMNDWIKLSGQNTITSTKCNFSSLLKLVYBEIKLIRA-EKENTSSWVEVDSFPPFKA 126
Db 76 YGQKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCCKWAESGRFYPFLET 135
QY 127 QIGPPEVHLEADKAIVTHISPGTK-----DSVMWALDGLSFTYSLLIWKNSSGVE 177
Db 136 QIGPPEVALTTDEKISVVLTAPEKWRNPEDLPVSMQQLYSNLKYNVSLNLTGKSNRTWS 195
QY 178 ERIENIYSHKIYK--LSPETTYCLKVAALTSWKIGVYSPVHCITVENE----- 228
Db 196 QCVTN-----HTLVLTWLEPTLYCVHVSFVPGPPRAQPSKQKARTLKQSSBFKAKI 251
QY 229 -----LPPPENIEVSQONQYVLKWDYTYANNTFQV-OWLHAFKLRNPNHLYKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLPSVMGYSIYRIYHVHGEKHPANLI----- 289
QY 283 CENVKTCQVPQNFQKGIYLLRVOASDGNNTSPWSEIEKPDTEI---QAPLLPPVFN 339
Db 290 -----LIYGNEDKRFV---PAEKIVINFTILNISDSKISHQDMSLLGKSDV 336
QY 340 RSLSDSFHYIYGAPQSGNTVPIDYPLIYEI-----IFWENTSNAERKIEKKTVDV 391
Db 337 SSLND-----POPSGNLRNPQBEIEVKHGLGYASHLMEIFCDSEENTGTSFTQBSL 388
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Db 136 QIGPPEVALTTDEKSI SVVLTAPEKWKRNPEDLFVSMQOQIYSLKYNVSVLNTKSNRTWS 195
Qy 178 ERIENIYSRHKIYK--LSPETTYCLKVKAAALTSWKIGVYSPVHCICKTTVENE----- 228
Db 196 QCVTN---HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSSEKQACARTLKQOSSEFKAKI 251
Qy 229 -----LPPENIEVSQONQYVLKWDYTYANMTFQV-OMLHAFKRNPGNHLKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRVIHVGEKHPANLI----- 289
Qy 283 CENVKTTQCVPFQNVOKGIYLLRVQASDGNNTSFWESEIKPDEI---QAFLLPPVFN 339
Db 290 -----LIYNEEDKRFV---PAEKVINFINITLNSDDSKISHQDMSLLGKSSDV 336
Qy 340 RSLSDSFHIYIGAPKOSGNTPTQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQSGNLPRPQBEVEVKHGLGYASHLMEIFCDSEBTEGTSTQOESL 388
Qy 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 13
US-10-636-716-34
; Sequence 34, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-10-636-716-34

Query Match 8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.le-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

Qy 11 LVLVAVGPM--VLSAAGGKNLKSPOKVEVDIIDNFILRNRSDESUG-NVTFSFDYQK 67
Db 18 LLLLLAAPGRAWPCVSGG--LPKANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
Qy 68 TGMNDWIKLSGCONITSTKCNFSSLLKLVYEEIKLRIR- EKENTSSWYEVDSFTPRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDEYHQYAKVKAIWGTKCSKWAESGRFYPLET 135
Qy 127 QIGPPREHLEARDKATVIHISPTK-----DSVMWALDGLSFTYSLLIWNKSSGVE 177
Db 136 QIGPPEVALTTDEKSI SVVLTAPEKWKRNPEDLFVSMQOQIYSLKYNVSVLNTKSNRTWS 195
Qy 178 ERIENIYSRHKIYK--LSPETTYCLKVKAAALTSWKIGVYSPVHCICKTTVENE----- 228
Db 196 QCVTN---HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSSEKQACARTLKQOSSEFKAKI 251
Qy 229 -----LPPENIEVSQONQYVLKWDYTYANMTFQV-OMLHAFKRNPGNHLKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRVIHVGEKHPANLI----- 289
Qy 283 CENVKTTQCVPFQNVOKGIYLLRVQASDGNNTSFWESEIKPDEI---QAFLLPPVFN 339
Db 290 -----LIYNEEDKRFV---PAEKVINFINITLNSDDSKISHQDMSLLGKSSDV 336
Qy 340 RSLSDSFHIYIGAPKOSGNTPTQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQSGNLPRPQBEVEVKHGLGYASHLMEIFCDSEBTEGTSTQOESL 388
Qy 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 14
US-10-636-716-36
; Sequence 36, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/943,087
; FILING DATE:
```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-36

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.le-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGKNLSPQKVEVDIIDNFILRWNRSDSVG-NVTFSPDYOK 67
DB 18 LLLLLAAPGWRAPCVSGG--LPKPANITFLSNKQVLTQWTPPEGLQGVKVTYTVQVPI 75
QY 68 TGMNDWIKLSCQNTSTKCNFSSLLKLVYBEIKLIRA-EKENTSSWYVDSTPPFRKA 126
DB 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCCKWAESGRFYFPLET 135
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMALDGLSFTYSLLIWKNSSGVE 177
DB 136 QIGPPEVALTTDEKSI SVLTAPKWRNPEDLPVSMQOIYSNLKNVSVLNTKSNRTWS 195
QY 178 ERIENIYSRHKYK--LSPETTYCLKVKKAALLTSWKIGVYSPVHCIKTTVENE----- 228
DB 196 QCVTN-----HTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARLTKDQSSSEFKAKI 251
QY 229 -----LPPPENIEVSQNTYLVKWDYTYANNTFQV-QWLHAFKLRNPGNHLYKWKQIPD 282
DB 252 IFWYVLP-----ISITV-----PLFSVMGYSIYRIVHVGKEKHPANLI----- 289
QY 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDTEI---QAFLLPPVFN 339
DB 340 RSLSDSFHIYGAPKQSGNTPVQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
QY 392 --TVPNLKPLTVY 402
DB 389 SRTIPDPKTVIEY 401

RESULT 15
US-10-636-716-38
; Sequence 38, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-38

```

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Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.le-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGKNLSPQKVEVDIIDNFILRWNRSDSVG-NVTFSPDYOK 67
DB 18 LLLLLAAPGWRAPCVSGG--LPKPANITFLSNKQVLTQWTPPEGLQGVKVTYTVQVPI 75
QY 68 TGMNDWIKLSCQNTSTKCNFSSLLKLVYBEIKLIRA-EKENTSSWYVDSTPPFRKA 126
DB 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCCKWAESGRFYFPLET 135
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMALDGLSFTYSLLIWKNSSGVE 177
DB 136 QIGPPEVALTTDEKSI SVLTAPKWRNPEDLPVSMQOIYSNLKNVSVLNTKSNRTWS 195
QY 178 ERIENIYSRHKYK--LSPETTYCLKVKKAALLTSWKIGVYSPVHCIKTTVENE----- 228
DB 196 QCVTN-----HTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARLTKDQSSSEFKAKI 251
QY 229 -----LPPPENIEVSQNTYLVKWDYTYANNTFQV-QWLHAFKLRNPGNHLYKWKQIPD 282
DB 252 IFWYVLP-----ISITV-----PLFSVMGYSIYRIVHVGKEKHPANLI----- 289
QY 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDTEI---QAFLLPPVFN 339
DB 290 -----LIYGNFEDKRFV----PAEKIVINFTILNISDDSKISHQDMSLGKSSDV 336
QY 340 RSLSDSFHIYGAPKQSGNTPVQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
DB 337 SSLND-----PQPSGNLRPPQEEVVKHLYASHLMEIFCDSEENTEGTSFTQESL 388
QY 392 --TVPNLKPLTVY 402

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Db           |:| | : |  
              389 SRIPDKTVIEY 401

Search completed: January 17, 2006, 07:36:14  
Job time : 18.7109 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 07:06:37 ; Search time 23.4755 Seconds  
(without alignments)  
1643.539 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427  
Perfect score: 2141  
Sequence: 1 GKNLKSPQKVEVDIIDNFI.....AHTMDEKLNKSSVPSDAVCE 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	557	2 A32694	interferon alpha/b
2	1384.5	64.7	560	2 S27387	interferon alpha r
3	966	45.1	590	2 A45283	interferon alpha/b
4	220	10.3	325	2 A47003	cytokine receptor
5	217.5	10.2	349	2 J06311	interferon recepto
6	199	9.3	332	2 A49947	interferon gamma r
7	148	6.9	337	2 I38500	interferon gamma r
8	123.5	5.8	1443	2 I50600	neogenin - chicken
9	123	5.7	1375	2 T13822	frazzled gene prot
10	123	5.7	1526	2 T13823	frazzled gene prot
11	122.5	5.7	1451	2 S42167	190K protein. - hum
12	120	5.6	2057	2 F90109	splicing factor Pr
13	118	5.5	489	2 A31555	interferon gamma r
14	118	5.5	981	2 S15604	receptor-like tyro
15	118	5.5	1005	2 S49015	receptor tyrosine
16	117.5	5.5	1383	2 A36080	insulin receptor p
17	117.5	5.5	1427	2 I51669	tumor suppressor
18	117.5	5.5	1585	2 T19121	probable protein-t
19	117	5.5	817	2 A48721	titin, muscle - ch
20	115.5	5.4	658	2 T16040	hypothetical prote
21	115	5.4	26926	1 I38344	titin, cardiac mus
22	113	5.3	1450	2 A44027	165K myofibrillar
23	113	5.3	1615	2 B49502	protein-tyrosine-p
24	113	5.3	1767	2 A49502	protein-tyrosine-p
25	111.5	5.2	1896	2 T08851	Down syndrome cell
26	111	5.2	6831	2 A88852	protein unc-22 (im
27	111	5.2	6839	2 S57242	twitchin (similar
28	111	5.2	7160	2 T27935	hypothetical prote
29	110.5	5.2	1898	2 S46216	leukocyte antigen-

30	110	5.1	1912	2 A56178	protein-tyrosine-p
31	109.5	5.1	575	2 A49667	interleukin-10 rec
32	109.5	5.1	657	2 D81308	probable integral
33	109	5.1	416	2 T25036	hypothetical prote
34	108.5	5.1	2215	2 T00348	Lrll protein - mou
35	108	5.0	991	2 I78843	receptor protein-t
36	107.5	5.0	1372	2 A34157	insulin receptor p
37	105.5	4.9	574	2 D81372	probable outer-mem
38	105.5	4.9	878	1 A40051	interleukin-3 rece
39	105.5	4.9	1825	2 C88400	protein H19M22.1 f
40	105.5	4.9	1825	2 T32828	hypothetical prote
41	105	4.9	56	2 S41602	interferon alpha r
42	105	4.9	1027	2 B90527	atp-binding protei
43	104.5	4.9	1447	2 A54100	tumor suppressor p
44	104	4.9	896	1 A35782	cytokine receptor
45	104	4.9	1239	1 A32579	neuroglian - fruit

ALIGNMENTS

RESULT 1

A32694  
interferon alpha/beta receptor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: A32694; S17112  
R:Uze, G.; Lutfalla, G.; Gresser, I.  
Cell 60, 225-234, 1990  
A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse cell  
A:Reference number: A32694; MUID:90124632; PMID:2153461  
A:Accession: A32694  
A:Molecule type: mRNA  
A:Residues: 1-557 <UZE>  
A:Cross-references: UNIPROT:P17181; UNIPARC:UPI000002D51B; GB:J03171; NID:g184645; PIDN:  
R:Lutfalla, G.  
submitted to the EMBL Data Library, July 1991  
A:Description: The structure of the human interferon alpha/beta receptor gene.  
A:Reference number: S17112  
A:Accession: S17112  
A:Molecule type: DNA  
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>  
A:Cross-references: UNIPARC:UPI0000179801; EMBL:X60459; NID:g32671  
C:Genetics:  
A:Gene: GDB:IFNARI; IFNAR; IFRC  
A:Cross-references: GDB:I20078; OMIM:107450  
A:Map position: 21q22.1-21q22.1  
A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3  
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F:1-21/Domain: transmembrane #status predicted <TRN1>  
F:437-455/Domain: transmembrane #status predicted <TRN2>  
F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate (As

Query Match	100.0%	Score	2141	DB 2	Length	557	
Best Local Similarity	100.0%	Pred. No.	3.9e-153				
Matches	401	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	GKNLKSPQKVEVDIIDNFI	LRNRSDESGVNTFSFDYQKTGMNDNWKLSGCQNTSTK	60			
Db	27	GKNLKSPQKVEVDIIDNFI	LRNRSDESGVNTFSFDYQKTGMNDNWKLSGCQNTSTK	86			
Qy	61	CNFSLLKLVYEEIKLRIRAEKENTSSWYVDSTFPPRKAQIGPPEVHLEADKAIVIH	120				
Db	87	CNFSLLKLVYEEIKLRIRAEKENTSSWYVDSTFPPRKAQIGPPEVHLEADKAIVIH	146				
Qy	121	SPGTKDSVMWALDGLSFTYSLLIWNKSSGVSEERIENISRHKIYKLSPTTYCLVKVKAAL	180				
Db	147	SPGTKDSVMWALDGLSFTYSLLIWNKSSGVSEERIENISRHKIYKLSPTTYCLVKVKAAL	206				
Qy	181	LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNTVVLKWDITYANNITFOVQWLHAF	240				
Db	207	LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNTVVLKWDITYANNITFOVQWLHAF	266				



QY 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEIEKFD 300  
Db KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEIEKFD 326  
QY 301 EIQAFLLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKII 360  
Db EIQAFLLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKII 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 401  
Db KKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 427  
RESULT 2  
S27387  
Interferon alpha receptor type 1 precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
R;Accession: S27387; S33770  
R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.  
FEBS Lett. 313, 255-259, 1992  
A;Title: Specific antiviral activities of the human alpha interferons are determined at  
A;Reference number: S27387; MUID:93076908; PMID:1446745  
A;Accession: S27387  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-560 <MOU>  
A;Cross-references: UNIPROT:Q04790; UNIPARC:UPI0000012698; EMBL:X68443; NID:g431; PIDN:Q  
A;Experimental source: MDBK cells  
R;Lim, J.K.; Langer, J.A.  
Biochim. Biophys. Acta 1173, 314-319, 1993  
A;Title: Cloning and characterization of a bovine alpha interferon receptor.  
A;Reference number: S33770; MUID:93305725; PMID:8318540  
A;Accession: S33770  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-421, 'V', 423-560 <LIM>  
A;Cross-references: UNIPARC:UPI00000167C2D; EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PI  
A;Experimental source: lung  
A;Keywords: antiviral; cytokine receptor; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <Sig>  
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>  
Query Match 64.7%; Score 1384.5; DB 2; Length 560;  
Best Local Similarity 64.0%; Pred. No. 2.7e-96;  
Matches 258; Conservative 62; Mismatches 78; Indels 5; Gaps 5;  
QY 3 NLKSPQKVEVDIIDDNFIPLRNWSDSVGNVTFSDYQKTMGNWIKLSCQNTSTKCN 62  
Db NLK-PENVEITHIIDDNFIPLRNWSDSVGNVTFSDYQKTMGNWIKLSCQNTSTKCN 85  
QY 63 FSSILKL-NVYEEIKLRRAEK-ENTSSWYVDSTFPERKAOIGPPEVHLEAEKAIYHI 120  
Db FSSVELENPEKELIRABEGNNTSTWYVEVPVFPPEAQIGPPDVHLEAEKAIILSI 145  
QY 121 S-PGTQSDVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPTTYCLKVKAA 179  
Db SPGTQSDINWADRSSFRSVVIWKNSLSLEERTETVYPEDKIYKLSPTTYCLKVKA 205  
QY 180 LLTSWKIGVYSPVHCIKTTVENLPPENIEVSQVQNYVYLKWDYTYANNMTFQVQMLHAF 239  
Db LLTSWKIGVYSPVHCIKTTVENLPPENIEVSQVQNYVYLKWDYTYANNMTFQVQMLHAF 265  
QY 240 LKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEIEKFD 299  
Db LKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEIEKFD 325  
QY 300 TEIQAFLLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKI 358  
Db TEIQAFLLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKI 385  
QY 359 IEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 401  
Db IEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 427

Db 386 LEKRTNFIFDLKPLTVYCVKARALIENDRRNKGSSFSFSDTVC 428  
RESULT 3  
A45283  
Interferon alpha/beta receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
R;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429  
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.  
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992  
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp  
A;Reference number: A45283; MUID:92262522; PMID:1533935  
A;Accession: A45283  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-590 <UZE>  
A;Cross-references: UNIPROT:P33896; UNIPARC:UPI00000027A2F; GB:M89641; NID:g194111; PIDN:A  
R;Lutfalla, G.; Uze, G.  
Gene 148, 343-346, 1994  
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq  
A;Reference number: I48423; MUID:95047447; PMID:7958966  
A;Accession: I48423  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 118-125 <RES>  
A;Cross-references: UNIPARC:UPI0000000524; EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PI  
A;Accession: I48424  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 127-224 <RES>  
A;Cross-references: UNIPARC:UPI0000000525; EMBL:U06238; NID:g497104; PIDN:AAAC01749.1; PI  
A;Accession: I48425  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 243-264 <RES>  
A;Cross-references: UNIPARC:UPI0000000526; EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PI  
A;Accession: I48426  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 265-375 <RES>  
A;Cross-references: UNIPARC:UPI0000000527; EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PI  
A;Accession: I48427  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 397-424 <RES>  
A;Cross-references: UNIPARC:UPI0000000528; EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PI  
A;Accession: I48428  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 426-445 <RES>  
A;Cross-references: UNIPARC:UPI0000000529; EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PI  
A;Accession: I48429  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 473-590 <RES>  
A;Cross-references: UNIPARC:UPI000000052A; EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PI  
C;Genetics:  
A;Gene: IFNAR  
A;Introns: 177/3; 331/1  
C;Keywords: cytokine receptor; transmembrane protein  
Query Match 45.1%; Score 966; DB 2; Length 590;  
Best Local Similarity 47.8%; Pred. No. 8.3e-65;  
Matches 192; Conservative 71; Mismatches 130; Indels 10; Gaps 4;  
QY 1 GNKLSQKVEVDIIDDNFIPLRNWSDSVGNVTFSDYQKTMGNWIKLSCQNTSTK 60  
Db GNKLSQKVEVDIIDDNFIPLRNWSDSVGNVTFSDYQKTMGNWIKLSCQNTSTK 85  
QY 61 CNPSSLKNVYEEIKLRIRAEKEN-TSSWYVDSTFPERKAOIGPPEVHLEAEKAIYHI 119  
Db CNPSSLKNVYEEIKLRIRAEKEN-TSSWYVDSTFPERKAOIGPPEVHLEAEKAIYHI 145



Matches	89;	Conservative	60;	Mismatches	194;	Indels	61;	Gaps	19;
Qy	6	SPOKVEVDIIDNFI-LRWNR--SDESVGNVTFSDYQKTGMNDWIKLSCQONITSTKCN	62						
Db	427	APRDVATLSTFRILRTWRTPVSDPGDNLTYISIFVTKBG---INRRVEN-TSRPGE	481						
Qy	63	FSSKLNVYEIKLRPAEKENTSSWYEVDSFPPFKAQIGPPEVHLEAEDKAIVIHISP	122						
Db	482	TQVMIQMLPETVYVFRVVAQNKHGHE--SSAPLKVAT--QPEVQLPGPAPNIRAYGS	537						
Qy	123	GTKDSVNWAL----DGLSFYSLIWKNSGVEERIENIYSRKIKVLSPETTYCLAKVA	178						
Db	538	PTSVTYTWETPLSGNGEIQNYKLYYNEKGQDSQDDVAVGLSTYITGLKXYTYSFRVA	597						
Qy	179	ALLTSWKIGYVSPHCKITTVENELPPPENVSVQN-QNYVLKWDYTYANMTFQVQMLH	237						
Db	598	--YNHGPGVSTQDVVVRTLSDVPSAAPQNLTEARNSKIMLHWQPPA-----	645						
Qy	238	AFLLKRNPGNHL-----YKWKQIIPDCENVKTTQCVPQNVFO--KGI-----YLLRVQASD	285						
Db	646	-----GTHSGQITGYKIRYKVRKSDVTESVGGTQFLQIEGLERGTEYNFRIAAMT	698						
Qy	286	GNNT--SFWSEBIKDFTEIOAFLPPV---FNIRISLSDSFHYIGAPKQSGNTPVIODY	339						
Db	699	VNGTGPATDWVSAETPESDLDSESRVEVPSLHVRPLVTSI-VVSWTPPENQNI-VVRGY	756						
Qy	340	PLIYEIIFWENTSNAER-KIIEKTDVTVPNLKPLTYVCVKARA	382						
Db	757	AIGYGI-----GSPAQCTIKVDYKORYVTYITENLDPSSHYVITLKA	796						

RESULT 9  
T13822  
frizzled gene protein - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13822  
R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.  
Cell 87, 197-204, 1996  
A:Title: Frizzled encodes a *Drosophila* member of the DCC immunoglobulin subfamily  
A:Reference number: Z17780; MUID:97015076; PMID:8861904  
A:Accession: T13822  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1375 <KOL>  
A:Cross-references: UNIPROT:Q94537; UNIPARC:UPI00000422DD; EMBL:U71001; NID:916;  
C:Genetics:  
A:Gene: frizzled  
A:Cross-references: FlyBase:FBgn0011592  
A:Map position: 2  
C:Function:  
A:Description: may function in vivo as a receptor or component of a receptor me

Query Match	5.7%;	Score 123;	DB 2;	Length 1375;
Best Local Similarity	16.3%;	Pred. NO. 0.58;		
Matches 101;	Conservative	68;	Mismatches 184;	Indels 268; Gaps 22;
Qy	1	GKNLKS-----PQKVEVDIIDNFI-LRW-----	-----NRSDSVSG	31
Db	448	GKPLDGLQARLPSPQRLVAQIKVRSFVTLWVBEPLQAGDVVVVYVYKMNNSREQ	507	
Qy	32	NVTFSPDYKGTGMNWKLSGCGNITSTKCNPS-----	-----LKNVYEEIKLR	77
Db	508	MVTKSHDDQGVNIQSLLPGETYQFRVEANTNFCSGASSAPLEVSTQPEVNIAGPPRNFE	567	
Qy	78	-IABKXENTSSTWYE-----	-----VD	92
Db	568	YAKSHKEIYVYKKEEPTVTNGEILKYRVVYSENDSGADLYHDSTALEAVLTLPHPHTDYVI	627	
Qy	93	SFTPFKRAQIG-----	-----PPEVHLE-AEDKAIVIHISPTKDSVMWALD	133
Db	628	SVYFPFNRNGMGDSABIRVKVTFSTPSEPPNNVTLEVTSSSITVTHWEPAAEDRNGQIT	687	

```

Qy 188 VYSPVCHIKTTVENELP-----PPENIEVSQVQNYVLKW 222
      |||
Db 896 -----NTLENDLDETOVPGKPIWISHPGANNIALHWGPPQHPEIKI--RNYVLGW 944
      |||
Qy 223 -----DY-----224
      ||
Db 945 GRGIPDENTIELKETERYHILKNLESNMWYVSLRARNVKGDPPIYDNIKTRDEEPVDA 1004
      ||
Qy 225 -----TYANNTFQVQLHAFLEKRN-----PGNHLKYWKQIPD 256
      |||
Db 1005 PTPLEVPVGLRAITMSSSSIVWYIDITMLNKNQHVTDNRHYTVSYGITGSNRYR-----1059
Qy 257 CENVKTTQCVPFQNVFGKGYLLRVOASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSL 316
      |||
Db 1060 -HNTTDLNCHI-NDLRPNTQYEFANVKVKKRRSSWSKSVLNTYQNVVPTPP-----1110
      |||
Qy 317 SDSPHIYIGAPKQSGNTPVIQDVP-----LIYEIIFWENTSNAER-----KILBKKT 363
      |||
Db 1111 --REVTVRLDEMNPPTVIVQWIPPKHTLGITGYNIIYYTDTTKRDRDWSVEAFAGEET 1167
      |||
Qy 364 DVTVPNLKPLTVYCVKRAHT 384
      |||
Db 1168 MLMPLNLKPYTTYFYFKVQART 1188
      |||

RESULT 11
S42167
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S42167
R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.
J. Cell Sci. 106, 319-330, 1993
A:Title: The globular head domain of titin extends into the center of the sarco-
A:Reference number: S42166; MUID:94095665; PMID:7505783
A:Accession: S42167
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1451 <V>N>
A:Cross-references: UNIPROT:P52179; UNIPARC:UPI000012PB8B; EMBL:X69090; NID:9400
C:Superfamily: skeleton

Query Match          5.7%; Score 122.5; DB 2; Length 1451;
Best Local Similarity 19.8%; Pred. No. 0.68;
Matches 91; Conservative 66; Mismatches 181; Indels 121; Gaps 21;

Qy 17 DNFILRNWRSDSEVGN--VTFSPFYQTKGMNDWIKLSCQCNITSTKCNFSLKLVNTHFI 74
      |||

```

[illegible]



```
Qy 162 KIYKLSPTTYCLVKVKAALLTSWIKGVSPVH-----CIKTTVENELPP----- 205
Db 310 GFFKASPHSQCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTWACTRP 359
Qy 206 ---PENIEVSQONQNYVLKW-----DYTYANMTFFQVWLHAFLEKRNPGNHLKYWK 252
Db 360 PSAPRNALSNVNETSVFLEWIPADTGGGKDVSYIILCKKN-SHAGVCECGGHR--- 415
Qy 253 QIPDCENVKTTQCVPPQNVFGKIYLLRVQASDGNNTSFWSSEIKFDTETIOAFLPPVFN 312
Db 416 -----YLPQOIGLKNKTSVMWADPLAHTNYTF-----EIEA-----VNG 448
Qy 313 IRSLSDSFHHIYG---APKQSGNTPVIQ-----DYP-----LIYEIIF 347
Db 449 VSDLSPGTRQVSVNVTNQAAPSPVTVNVKKGIAKNSISLSWQEPDRPNGLIILEYEIKY 508
Qy 348 WENTSNAERKLIIE-KKTDVTPVNLKPLTVYCVKARAHT 384
Db 509 FEKQDQTSYTIKSKETTITAEGLKPAASVYVFOIRART 546
```

## RESULT 15

```
S49015
receptor tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S49015; S51602
R:Maisonnier, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777; PMID:7504232
A:Accession: S49015
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MAI>
A:Cross-references: UNIPROT:P54757; UNIPARC:UPI00000508E8; EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
A:Accession: S51602
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305, 'G', 359-1005 <MA2>
A:Cross-references: UNIPARC:UPI0000175665; EMBL:S68026
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:675-941/Domain: protein kinase homology <KIN>
F:683-691/Region: protein kinase ATP-binding motif
```

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Query Match 5.5%; Score 118; DB 2; Length 1005;
Best Local Similarity 20.1%; Pred. No. 0.9;
Matches 92; Conservative 51; Mismatches 165; Indels 150; Gaps 21;

Qy 1 GNLUKSPQKVEVDII--DDNF-----ILRNKSDSEVGNT---FSFDYQKTGMNDW 47
Db 165 GRNIKDNQYIKIDTIAADESEFELDGRVMKLTVEVRDVGPLSKKGFYLAQFDVG---- 220
Qy 48 IKLSGQNITST-----KCNFSSLLNLYVEEIKLIRAEKENTSSWYFVDSFTPFKAQI 102
Db 221 ----ACIALSVRVYKKCPSVVRHLAVFPD-----TTGADSSQLLEVSQSVNHSVTD 271
Qy 103 GPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFYSLLIWNKSSGVVEERIENI-YSRH 161
Db 272 DPPKMHCSAEGELV---PIGKMC-----KAGYEKNGTCQVCRP 309
Qy 162 KIYKLSPTTYCLVKVKAALLTSWIKGVSPVH-----CIKTTVENELPP----- 205
Db 310 GFFKASPHSQCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTWACTRP 359
Qy 206 ---PENIEVSQONQNYVLKW-----DYTYANMTFFQVWLHAFLEKRNPGNHLKYWK 252
Db 360 PSAPRNALSNVNETSVFLEWIPADTGGGKDVSYIILCKKN-SHAGVCECGGHR--- 415
```

```
Qy 253 QIPDCENVKTTQCVPPQNVFGKIYLLRVQASDGNNTSFWSSEIKFDTETIOAFLPPVFN 312
Db 416 -----YLPQOIGLKNKTSVMWADPLAHTNYTF-----EIEA-----VNG 448
Qy 313 IRSLSDSFHHIYG---APKQSGNTPVIQ-----DYP-----LIYEIIF 347
Db 449 VSDLSPGTRQVSVNVTNQAAPSPVTVNVKKGIAKNSISLSWQEPDRPNGLIILEYEIKY 508
Qy 348 WENTSNAERKLIIE-KKTDVTPVNLKPLTVYCVKARAHT 384
Db 509 FEKQDQTSYTIKSKETTITAEGLKPAASVYVFOIRART 546
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Search completed: January 17, 2006, 07:19:44  
Job time : 25.4755 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 06:26:20 ; Search time 79 Seconds  
(without alignments)

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKNLSPQKQVEVDIIDNFI.....AHTMDKLKNSVFSVDAVCE 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	436	2 AAR14487	Aar14487 Soluble i
2	2141	100.0	436	2 AAR28495	Aar28495 Sequence
3	2141	100.0	436	6 ABU05090	Abu05090 Human exp
4	2141	100.0	436	6 ABU05092	Abu05092 Human exp
5	2141	100.0	436	6 ABU05098	Abu05098 Human exp
6	2141	100.0	557	2 AAR14488	Aar14488 Complete
7	2141	100.0	557	2 AAR11958	Aar11958 Human alp
8	2141	100.0	557	2 AAR28496	Aar28496 Sequence
9	2141	100.0	557	2 AAR42635	Aar42635 Human int
10	2141	100.0	557	6 ABU05091	Abu05091 Human exp
11	2141	100.0	557	6 ABU05095	Abu05095 Human exp
12	2141	100.0	557	6 ABU05094	Abu05094 Human exp
13	2141	100.0	557	6 ABU05107	Abu05107 Human exp
14	2141	100.0	557	6 ABU05099	Abu05099 Human exp
15	2141	100.0	557	6 ABU05106	Abu05106 Human exp
16	2141	100.0	557	6 ABU05097	Abu05097 Human exp
17	2141	100.0	557	6 ABU05093	Abu05093 Human exp
18	2141	100.0	557	6 ABU05100	Abu05100 Human exp
19	2141	100.0	575	8 ADR66319	Adr66319 Human pro
20	2141	100.0	575	8 ADR66661	Adr66661 Human pro
21	2138	99.9	441	9 ADV25067	Adv25067 INR1_T11
22	2137	99.8	557	2 AAR75356	Aar75356 Human IFN
23	2137	99.8	557	6 ABU05102	Abu05102 Human exp
24	2136	99.8	434	2 AAW21805	Aaw21805 Spliced-d

25	2136	99.8	434	6 ABU05104	Abu05104 Human exp
26	2136	99.8	557	2 AAW21804	Aaw21804 Transmembr
27	2136	99.8	557	6 ABU05103	Abu05103 Human exp
28	2136	99.8	575	3 AAB57094	Aab57094 Human pro
29	2136	99.8	575	4 AEG17294	Aeg17294 Novel hum
30	2136	99.8	575	6 ABU05096	Abu05096 Human exp
31	2132	99.6	436	2 AAR71723	Aar71723 IFN recepr
32	2132	99.6	436	6 ABU05101	Abu05101 Human exp
33	2124	99.2	631	8 ADK23579	Adk23579 Human IFN
34	2084	97.3	496	2 AAW21806	Aaw21806 Spliced-d
35	2084	97.3	496	6 ABU05105	Abu05105 Human exp
36	1559.5	72.8	458	8 ADH22370	Adh22370 Human rec
37	798	37.3	187	8 ADH22369	Adh22369 Human rec
38	228	10.6	273	6 ABR38950	Abr38950 Human AK1
39	226	10.6	273	6 ABR38949	Abr38949 Human AK1
40	225	10.5	220	5 AAU76911	Aau76911 Human cvt
41	225	10.5	220	8 ADS31753	Ads31753 Human CRF
42	225	10.5	220	8 ADS92755	Ads92755 Human CRF
43	225	10.5	273	6 ABR38944	Abr38944 Human AK1
44	225	10.5	476	5 AAU76912	Aau76912 Human CRF
45	225	10.5	476	6 AAE30845	Aae30845 Human CRF

ALIGNMENTS

RESULT 1  
AAR14487  
ID AAR14487 standard; protein; 436 AA.  
XX AC AAR14487;  
XX DT 16-JAN-1992 (first entry)  
XX DE Soluble interferon-alpha/beta receptor.  
XX KW IFN; autoimmune disease; graft rejection; histocompatibility.  
XX OS Homo sapiens.  
XX PN FR2657881-A.  
XX PD 09-AUG-1991.  
XX PF 05-FEB-1990; 90FR-00001298.  
XX PR 05-FEB-1990; 90FR-00001298.  
XX PA (EUBI-) LAB EURO BIOTECHNO.  
XX PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG;  
XX Uze G;  
XX WPI; 1991-319778/44.  
XX DR N-PSDB; AAQ14239.  
XX PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
XX used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
XX anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX PS Claim 2; Page 45; 52pp; French.  
XX CC The transmembrane and cytoplasmic domains of the native IFN receptor have  
XX been deleted to obtain a soluble, circulating form of the receptor.  
XX CC Potentially immunogenic epitopes have thus been eliminated. Derivatives  
XX obtained by substitution or deletion of this sequence are also claimed as  
XX are hybrid molecules comprising the soluble receptor (or deriv.) and an  
XX immunoglobulin such as IgG1. See also AAQ14240

Query Match 100.0%; Score 2141; DB 2; Length 436;  
Best Local Similarity 100.0%; Pred. No. 1.6e-184;  
SQ Sequence 436 AA;



XX (ZYCO-) ZYCOS INC.  
XX Chicz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1756; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 436 AA;

Query Match 100.0%; Score 2141; DB 6; Length 436;  
Best Local Similarity 100.0%; Pred. No. 1.6e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
DB 27 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSKLKNVYEEIKLRIRAEKENTSSWVEVDSFTPFRAQIGPPPVHLEADKAIVIH 120  
DB 87 CNFSSKLKNVYEEIKLRIRAEKENTSSWVEVDSFTPFRAQIGPPPVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 206  
QY 181 LTSWKIGVSPVHCITTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVQMLHAF 240  
DB 207 LTSWKIGVSPVHCITTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVQMLHAF 266  
QY 241 KENPGNHLVKKQIPDCENVKTKQCVFPQNVFKGILYLLRVAOSDGNNTSFWSSEIKPDT 300  
DB 267 KENPGNHLVKKQIPDCENVKTKQCVFPQNVFKGILYLLRVAOSDGNNTSFWSSEIKPDT 326  
QY 301 EQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTPVIQDYPLIYEIIFWNTSNARKEIIE 360  
DB 327 EQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTPVIQDYPLIYEIIFWNTSNARKEIIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSVFSDAVCE 427

RESULT 4  
ABU05092  
ID ABU05092 standard; protein; 436 AA.  
XX  
AC ABU05092;  
XX

DT 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #1758.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX Homo sapiens.  
XX WO200278524-A2.  
XX 10-OCT-2002.  
XX 28-MAR-2002; 2002WO-US009671.  
XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCOS INC.  
XX Chicz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1758; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 436 AA;

Query Match 100.0%; Score 2141; DB 6; Length 436;  
Best Local Similarity 100.0%; Pred. No. 1.6e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
DB 27 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSKLKNVYEEIKLRIRAEKENTSSWVEVDSFTPFRAQIGPPPVHLEADKAIVIH 120  
DB 87 CNFSSKLKNVYEEIKLRIRAEKENTSSWVEVDSFTPFRAQIGPPPVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 206

QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFOVQWLHAPL 240  
DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFOVQWLHAPL 266  
QY 241 KRNPGNHLKWKQIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
DB 267 KRNPGNHLKWKQIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYEIIFWENTSNABERKIE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYEIIFWENTSNABERKIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 5  
ABU05098  
ID ABU05098 standard; protein; 436 AA.  
XX AC ABU05098;  
XX AC  
XX 29-JAN-2003 (first entry)  
XX  
XX Human expressed protein tag (EPT) #1764.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US0059671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
XX 21-MAY-2001; 2001US-0292544P.  
XX 08-AUG-2001; 2001US-0310801P.  
XX 01-OCT-2001; 2001US-0326370P.  
XX 04-DEC-2001; 2001US-0336780P.  
XX 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chicx RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1764; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 436 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 436;  
Best Local Similarity 100.0%; Pred. No. 1.6e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLKSPOKVEVDIIDDNFILRNRSDESQNVTFSPDYQKTGMNWKLSGCQNITSTK 60  
DB 27 GKNLKSPOKVEVDIIDDNFILRNRSDESQNVTFSPDYQKTGMNWKLSGCQNITSTK 86  
QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVIH 120  
DB 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFOVQWLHAPL 240  
DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFOVQWLHAPL 266  
QY 241 KRNPGNHLKWKQIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
DB 267 KRNPGNHLKWKQIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYEIIFWENTSNABERKIE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYEIIFWENTSNABERKIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 6  
AAR14488  
ID AAR14488 standard; protein; 557 AA.  
XX AC AAR14488;  
XX AC  
XX 16-JAN-1992 (first entry)  
XX  
XX Complete interferon-alpha/beta receptor.  
XX  
XX IFN; autoimmune disease; graft rejection; histocompatibility.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Domain 437..457  
FT /label= transmembrane  
FT Domain 458..557  
FT /label= cytoplasmic  
XX  
XX FR2657881-A.  
XX  
XX 09-AUG-1991.  
XX  
XX 05-FEB-1990; 90FR-00001298.  
XX  
XX 05-FEB-1990; 90FR-00001298.  
XX (EUBI-) LAB EURO BIOTECHNO.  
XX  
XX Bid P, Gresseer I, Lutfalla G, Meyer P, Mogensen KE, Tovey MG;

PI Ze G;  
XX WPI; 1991-319778/44.  
DR N-PSDB; AAQ14240.  
XX  
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
PT used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
PT anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX  
PS Disclosure; Page 47; 52pp; French.  
XX  
XX The invention covers derivatives of the interferon-alpha and/or beta  
CC receptor obtained by deleting the transmembrane and cytoplasmic domains  
CC of the native receptor or by substitution. Potentially immunogenic  
CC epitopes are eliminated and the deriv. can be secreted from transformed  
CC cells. Soluble deriv.s block the activity of IFN alpha/beta and can be  
CC used to treat autoimmune diseases or to inhibit graft rejection. See also  
CC AAQ14239  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILNRSDSVGNVTFSDYQKTMNDWIKLGGCONITSTK 60  
DB 27 GKNLSPQKVEVDIIDDNFILNRSDSVGNVTFSDYQKTMNDWIKLGGCONITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEAEDKAIVIH 120  
DB 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEAEDKAIVIH 146  
QY 121 SPGTQDSVMWALDGLSFTYSLIWKNSGVEERIEIYSRHKIYKLSPTTTCVLYKAAL 180  
DB 147 SPGTQDSVMWALDGLSFTYSLIWKNSGVEERIEIYSRHKIYKLSPTTTCVLYKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240  
DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266  
QY 241 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWESEIKFDT 300  
DB 267 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWESEIKFDT 326  
QY 361 KKTDTVTPNLKPLTVYCVKARHTWDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTPNLKPLTVYCVKARHTWDEKLNKSSVFSDAVCE 427

RESULT 7  
AAR11958  
ID AAR11958 standard; protein; 557 AA.  
XX  
AC AAR11958;  
XX  
DT 18-JUL-1991 (first entry)  
XX  
DE Human alpha-interferon receptor protein.  
XX  
DE Human alpha IFN; IFN agonists; antiviral; anti tumour agent;  
KW drug targetting.  
XX  
XX Homo sapiens.  
XX  
FH Key  
FT Peptide  
FT 1. .27  
XX /label= signal peptide

PN WO9105862-A.  
XX  
PD 02-MAY-1991.  
XX  
PF 20-OCT-1989; 89PR-00013770.  
XX  
PR 20-OCT-1989; 89PR-00013770.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
XX Mogensen K, Lutfalla G, Gresser I;  
PI WPI; 1991-148740/20.  
DR N-PSDB; AAQ11701.  
XX  
XX New human alpha-interferon receptor protein - useful for testing  
PT interferon agonists and in treatment or diagnosis.  
XX  
PS Disclosure; Fig 4; 30pp; French.  
XX  
CC This recombinant human alpha interferon (IFN) receptor protein is useful  
CC for the testing of IFN agonists and for treatment and diag- nosis of  
CC viral diseases and tumours. Antibodies raised against this protein can be  
CC used for blocking the receptor when required, eg where overexpression of  
CC alpha-IFN is harmful. The Abs are also useful for eg drug targetting.  
CC Variants of the protein, having residue 164 (Thr) replaced by Arg and an  
CC Asp inserted between residues 479 and 480, are also useful  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILNRSDSVGNVTFSDYQKTMNDWIKLGGCONITSTK 60  
DB 27 GKNLSPQKVEVDIIDDNFILNRSDSVGNVTFSDYQKTMNDWIKLGGCONITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEAEDKAIVIH 120  
DB 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEAEDKAIVIH 146  
QY 121 SPGTQDSVMWALDGLSFTYSLIWKNSGVEERIEIYSRHKIYKLSPTTTCVLYKAAL 180  
DB 147 SPGTQDSVMWALDGLSFTYSLIWKNSGVEERIEIYSRHKIYKLSPTTTCVLYKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240  
DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266  
QY 241 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWESEIKFDT 300  
DB 267 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWESEIKFDT 326  
QY 301 EIQAFLLPPVFNIRSLSDSFHYIGAPKSGNTPTVQDYPLIYELIIFWNTSNAERKII 360  
DB 327 EIQAFLLPPVFNIRSLSDSFHYIGAPKSGNTPTVQDYPLIYELIIFWNTSNAERKII 386  
QY 361 KKTDTVTPNLKPLTVYCVKARHTWDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTPNLKPLTVYCVKARHTWDEKLNKSSVFSDAVCE 427

RESULT 8  
AAR28496  
ID AAR28496 standard; protein; 557 AA.  
XX  
AC AAR28496;  
XX  
DT 25-MAR-2003 (revised)  
DT 31-MAR-1993 (first entry)  
XX  
DE Sequence of a soluble form of the interferon (IFN) receptor with a high

DE affinity for IFN-alpha and -beta.  
 XX Interferon receptor; alpha-interferon; beta-interferon.  
 KW Synthetic.  
 OS WO9218626-A1.  
 PN 29-OCT-1992.  
 PD 17-APR-1991; 91WO-FR000318.  
 PF 17-APR-1991; 91WO-FR000318.  
 PP 17-APR-1991; 91WO-FR000318.  
 PR (EUBI-) LAB EURO BIOTECHNOLOGIE.  
 XX Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
 PI Uze G;  
 XX WPI: 1992-382110/46.  
 DR N-PSDB; AAQ30533.  
 XX Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
 PT useful as immunosuppressants, for treating autoimmune diseases and  
 PT transplant rejection.  
 XX Claim 3; Fig 2; 58pp; English.  
 XX DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
 CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
 CC primers and cloned cDNA as template. For example, bacteriophage lambda  
 CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
 CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.  
 CC AAR28496 represents the complete receptor. AAR28495 lacks the  
 CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
 CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
 CC diseases and graft rejection. They lack the toxic side-effects of known  
 CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX Sequence 557 AA;  
 SQ Query Match 100.0%; Score 2141; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-184; Mismatches 0; Indels 0; Gaps 0;  
 Matches 401; Conservative 0;  
 QY 1 GNKLSQKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTGMNDNWKLSGQNITSTK 60  
 DB 27 GNKLSQKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTGMNDNWKLSGQNITSTK 86  
 QY 61 CNFSSKLNVYBEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 120  
 DB 87 CNFSSKLNVYBEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 146  
 QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
 DB 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
 QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVWLHAPL 240  
 DB 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVWLHAPL 266  
 QY 241 KNPNGHLYKWQIQIPDCENVKTTQCVFPQNVQKGIYLLRQASQGNNTSFWSBEIKFTD 300  
 DB 267 KNPNGHLYKWQIQIPDCENVKTTQCVFPQNVQKGIYLLRQASQGNNTSFWSBEIKFTD 326  
 QY 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKSGNTPTVQDPLIYELIPWENTSNAERKIE 360  
 DB 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKSGNTPTVQDPLIYELIPWENTSNAERKIE 386  
 QY 361 KKTDTVFNLPKLTIVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
 DB 387 KKTDTVFNLPKLTIVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 9  
 AAR42635  
 ID AAR42635 standard; protein; 557 AA.  
 XX AAR42635;  
 AC AAR42635;  
 XX 25-MAR-2003 (revised)  
 DT 20-APR-1994 (first entry)  
 XX Human interferon receptor.  
 DE IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; interferon-alpha-beta.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Domain 1..436  
 FT /label= extracellular domain  
 FT /note= "soluble, immunogenic form of IFN-R"  
 XX EP563487-A1.  
 XX 06-OCT-1993.  
 XX 31-MAR-1992; 92EP-00400902.  
 XX 31-MAR-1992; 92EP-00400902.  
 XX (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 XX Benoit P, Meyer F, Maguire D, Plavec I, Tovey MG;  
 XX WPI: 1993-312951/40.  
 DR P-PSDB; AAR42635.  
 XX Monoclonal antibody to human interferon type-I receptor - having  
 PT neutralising activity against human type I interferon, used for therapy  
 PT and diagnosis.  
 XX Disclosure; Fig 3; 21pp; English.  
 XX Monoclonal antibodies produced against soluble forms of the human  
 CC interferon alpha-beta receptor based on the full-length human IFN-R  
 CC sequence are claimed. The antibodies are useful for treatment and  
 CC prophylaxis of disorders involving cell proliferation and/or viral  
 CC infection. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 557 AA;  
 SQ Query Match 100.0%; Score 2141; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-184; Mismatches 0; Indels 0; Gaps 0;  
 Matches 401; Conservative 0;  
 QY 1 GNKLSQKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTGMNDNWKLSGQNITSTK 60  
 DB 27 GNKLSQKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTGMNDNWKLSGQNITSTK 86  
 QY 61 CNFSSKLNVYBEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 120  
 DB 87 CNFSSKLNVYBEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 146  
 QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
 DB 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
 QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVWLHAPL 240  
 DB 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVWLHAPL 266

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QY 241 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIGYLLRVQASDGNNTSFSEIEIKFDT 300
DB 267 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIGYLLRVQASDGNNTSFSEIEIKFDT 326
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIE 360
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIE 386
QY 361 KKTDTVTPNLKPLTVYCVKARAHMDEKLNKSSVFSDAVCE 401
DB 387 KKTDTVTPNLKPLTVYCVKARAHMDEKLNKSSVFSDAVCE 427

RESULT 10
ABU05091
ID ABU05091 standard; protein; 557 AA.
XX AC ABU05091;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1757.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX PS Example 2; SEQ ID NO 1757; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
```

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CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 557 AA;
Query Match 100.0%; Score 2141; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.2e-184;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLAKSPQKVEVDIIDDNFIILWNRSDSVGNVTFSDYQKTMGNWIKLSGCONITSTK 60
DB 27 GKNLAKSPQKVEVDIIDDNFIILWNRSDSVGNVTFSDYQKTMGNWIKLSGCONITSTK 86
QY 61 CNFSSILKLNVEEIKLIRAEKENTSSWYEVDSTFPPFRAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSILKLNVEEIKLIRAEKENTSSWYEVDSTFPPFRAQIGPPEVHLEADKAIVIH 146
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSGVBERIENIYSRHKIYKLSPTTYCLKYKAAL 180
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNKSGVBERIENIYSRHKIYKLSPTTYCLKYKAAL 206
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQVQNVYLVKWDYTYANNMTFOVQWLHAF 240
DB 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQVQNVYLVKWDYTYANNMTFOVQWLHAF 266
QY 241 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIGYLLRVQASDGNNTSFSEIEIKFDT 300
DB 267 KNPNGNHLKWKQIPDCENVKTTQCVFPQNVFKGIGYLLRVQASDGNNTSFSEIEIKFDT 326
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIE 360
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIE 386
QY 361 KKTDTVTPNLKPLTVYCVKARAHMDEKLNKSSVFSDAVCE 401
DB 387 KKTDTVTPNLKPLTVYCVKARAHMDEKLNKSSVFSDAVCE 427

RESULT 11
ABU05095
ID ABU05095 standard; protein; 557 AA.
XX AC ABU05095;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1761.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
```



DR WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX  
PS Example 2; SEQ ID NO 1761; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184; Indels 0; Gaps 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILWRNSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 60  
DB 27 GKNLSPQKVEVDIIDDNFILWRNSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 120  
DB 87 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSVQNYVLRWDYTYANNMTFOVWLHAPL 240  
DB 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSVQNYVLRWDYTYANNMTFOVWLHAPL 266  
QY 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWSEBIKFTT 300  
DB 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWSEBIKFTT 326  
QY 301 ETQAFLLPVPFNIRSLDSFHYIGAPKQSGNTPVTDYPLIYEIIFWNTSNAERKIE 360  
DB 327 ETQAFLLPVPFNIRSLDSFHYIGAPKQSGNTPVTDYPLIYEIIFWNTSNAERKIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSVFSDAVCE 427

RESULT 12  
ID ABU05094  
XX ABU05094 standard; protein; 557 AA.  
AC ABU05094;  
XX  
XX 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #1760.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
OS Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
XX  
XX 21-MAY-2001; 2001US-0292544P.  
XX  
XX 08-AUG-2001; 2001US-0310801P.  
XX  
XX 01-OCT-2001; 2001US-0326370P.  
XX  
XX 04-DEC-2001; 2001US-0336780P.  
XX  
XX 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCO INC.  
XX  
XX Chicx RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1760; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184; Indels 0; Gaps 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILWRNSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 60  
DB 27 GKNLSPQKVEVDIIDDNFILWRNSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 120  
DB 87 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSVQNYVLRWDYTYANNMTFOVWLHAPL 240  
DB 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSVQNYVLRWDYTYANNMTFOVWLHAPL 266

QY 241 KRNPGNHLKWKQIIPDCENVKTTQCVFQNVQKGIYLLRVQASDGNNTSFWSBEIKPDT 300  
DB 267 KRNPGNHLKWKQIIPDCENVKTTQCVFQNVQKGIYLLRVQASDGNNTSFWSBEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIIFWNTSNAERKITE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIIFWNTSNAERKITE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 13  
ID ABU05107  
XX AC ABU05107;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1773.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX DR WPI; 2003-040607/03.  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX PS Example 2; SEQ ID NO 1773; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKXLSPOKVEVDIIDDNPFILWNRSDSVGNVTSFDYQKTGMNDWIKLSCQNTITSTK 60  
DB 27 GKXLSPOKVEVDIIDDNPFILWNRSDSVGNVTSFDYQKTGMNDWIKLSCQNTITSTK 86  
QY 61 CNFSSILKLNVEBEIKLIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEASDKAIVIH 120  
DB 87 CNFSSILKLNVEBEIKLIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEASDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLIWKNSGVEBERIENYSRHKIYKLSPTTTCVQVLAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLIWKNSGVEBERIENYSRHKIYKLSPTTTCVQVLAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQMLHAF 240  
DB 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQMLHAF 266  
QY 241 KRNPGNHLKWKQIIPDCENVKTTQCVFQNVQKGIYLLRVQASDGNNTSFWSBEIKPDT 300  
DB 267 KRNPGNHLKWKQIIPDCENVKTTQCVFQNVQKGIYLLRVQASDGNNTSFWSBEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIIFWNTSNAERKITE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIIFWNTSNAERKITE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427  
RESULT 14  
ABU05099  
ID ABU05099 standard; protein; 557 AA.  
XX AC ABU05099;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1765.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX DR WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1765; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 266  
QY 241 KENPGNHLKWKQIIPDCENVKTTQCVFQNVFQKGIYLLRVQASDGNNTSFWSEIKFDT 300  
Db 267 KENPGNHLKWKQIIPDCENVKTTQCVFQNVFQKGIYLLRVQASDGNNTSFWSEIKFDT 326  
QY 301 EIQAFLPPVFNIRSLDSFHYIGAPKQSGNTPIQDYPLIYEIIFWENTSNAERKIIIE 360  
Db 327 EIQAFLPPVFNIRSLDSFHYIGAPKQSGNTPIQDYPLIYEIIFWENTSNAERKIIIE 386  
QY 361 KKTDTVTNPKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNPKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 427  
RESULT 15  
ABU05106  
ID ABU05106 standard; protein; 557 AA.  
XX  
AC ABU05106;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1772.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
XX  
XX 21-MAY-2001; 2001US-0292544P.  
XX  
XX 08-AUG-2001; 2001US-0310801P.  
XX  
XX 01-OCT-2001; 2001US-0326370P.  
XX  
XX 04-DEC-2001; 2001US-0336780P.  
XX  
XX 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chiciz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
XX cytoskeletal proteins, receptors or transcription factors), useful for  
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.  
XX  
XX Example 2; SEQ ID NO 1772; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
XX fragment of a kinase, phosphatase, protease, protease inhibitor,  
XX transporter, cytoskeletal protein, receptor or transcription factor. The  
XX polypeptide is useful as an immunogenic composition for eliciting in a  
XX mammal an immunogenic response directed against any of the purified  
XX polypeptide. The purified polypeptide, or the antibody that binds to this  
XX polypeptide, is useful for treating cancer. The polypeptide is also  
XX useful for identifying compounds that binds to a naturally processed  
XX class I or class II MHC-binding polypeptide. The polypeptides and  
XX polynucleotides are particularly useful for treating or preventing  
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
XX lymphoma or leukaemia. These are also useful for screening agents for  
XX treating the above mentioned diseases. This sequence represents an  
XX expressed protein tag (EPT) isolated from human tissue for translational  
XX profiling. Note: This sequence does not appear in the printed  
XX specification but was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 266  
QY 241 KENPGNHLKWKQIIPDCENVKTTQCVFQNVFQKGIYLLRVQASDGNNTSFWSEIKFDT 300

Db 267 KENPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFNSEIKFDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELFWNTSNAERKIIE 360  
Db 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELFWNTSNAERKIIE 386  
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 16  
ABU05097  
ID ABU05097 standard; protein; 557 AA.  
XX AC ABU05097;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1763.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX PS Example 2; SEQ ID NO 1763; 134pp; English.  
XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184; Mismatches 0; Indels 0; Gaps 0;  
Matches 401; Conservative 0;  
QY 1 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYQKTGMNDWIKLSCQNITSK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYQKTGMNDWIKLSCQNITSK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEARDKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEARDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENYSRHKIYKLSPTTCLVKYKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENYSRHKIYKLSPTTCLVKYKAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPPELVSVQNTYVLKWDYTYANNFTQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPELVSVQNTYVLKWDYTYANNFTQVQWLHAF 266  
QY 241 KENPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFNSEIKFDT 300  
Db 267 KENPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFNSEIKFDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELFWNTSNAERKIIE 360  
Db 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELFWNTSNAERKIIE 386  
QY 361 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 17  
ABU05093  
ID ABU05093 standard; protein; 557 AA.  
XX AC ABU05093;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1759.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX DR ftp.wipo.int/pub/published\_pct\_sequences



Db 267 KRNPGNHLKWKQIPDCENVKTTQCVPQNVFKGIIYLLRVQASDGNNTSFWSBEIKFPT 326  
Qy 301 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWNTSNAERKIIIE 360  
Db 327 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWNTSNAERKIIIE 386  
Qy 361 KKTDTVTPNPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTPNPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 427

RESULT 19  
ADR666319  
ID ADR666319 standard; protein; 575 AA.  
XX ADR666319;  
XX  
XX  
DT 02-DEC-2004 (first entry)  
DE Human prostatic carcinoma derived protein SEQ ID 173 #2.  
XX

XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.  
XX

OS Homo sapiens.

XX WO2004076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

PR 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.

PA (PILAR/) PILARSKY C.

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Xinzhong L, Staub E;

XX WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.

XX Claim 2; Page 653; 1607pp; German.

XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from

CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.

XX SQ Sequence 575 AA;

Query Match 100.0%; Score 2141; DB 8; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2.3e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPOKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTMGNWIKLSCQNITSTK 60  
Db 45 GKNLKSPOKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTMGNWIKLSCQNITSTK 104  
Qy 61 CNFSSLKLVYBEIKLRIRAEKENTSSWYEVDSFPPFKAQIGPPEVHLEAEDKAIVIH 120  
Db 105 CNFSSLKLVYBEIKLRIRAEKENTSSWYEVDSFPPFKAQIGPPEVHLEAEDKAIVIH 164  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENISRHKIYKLSPTTCLVKVKAAL 180  
Db 165 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENISRHKIYKLSPTTCLVKVKAAL 224  
Qy 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVNLYKWDYTYANNMTFQVQLHAF 240  
Db 225 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVNLYKWDYTYANNMTFQVQLHAF 284  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVPQNVFKGIIYLLRVQASDGNNTSFWSBEIKFPT 300  
Db 285 KRNPGNHLKWKQIPDCENVKTTQCVPQNVFKGIIYLLRVQASDGNNTSFWSBEIKFPT 344  
Qy 301 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWNTSNAERKIIIE 360  
Db 345 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWNTSNAERKIIIE 404  
Qy 361 KKTDTVTPNPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 401  
Db 405 KKTDTVTPNPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 445

RESULT 20

ADR666661

ID ADR666661 standard; protein; 575 AA.

XX ADR666661;

XX 02-DEC-2004 (first entry)

XX Human prostatic carcinoma derived protein SEQ ID 173 #3.

XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.

XX Homo sapiens.

XX WO2004076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

PR 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

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PA (PILA/) PILARSKY C.  
XX  
PI Hinemann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Kinzhong L, Staub E;  
XX  
DR WPI; 2004-553386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX

PS Claim 2; Page 1155; 1607pp; German.

XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.

XX Sequence 575 AA;  
SQ  
Query Match 100.0%; Score 2141; DB 8; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2.3e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKNLSPQKVEVDIIDDNFILRWNRSDSGVNVTFSDYQKTGMDNWKILSGCQNTSTK 60  
DB 45 GKNLSPQKVEVDIIDDNFILRWNRSDSGVNVTFSDYQKTGMDNWKILSGCQNTSTK 104  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEADKAIVIH 120  
DB 105 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEADKAIVIH 164  
QY 121 SPGTKDSVNMWALDGLSFTYSLIWKNSGVEERENIYSRHKIYKLSPTTYCLKVKAAL 180  
DB 165 SPGTKDSVNMWALDGLSFTYSLIWKNSGVEERENIYSRHKIYKLSPTTYCLKVKAAL 224  
QY 181 LTSWIKIGVSPVHCITKTVENELPPENIEVSQVQNYVYLKWDYTYANNFTFOVQWLHAF 240  
DB 225 LTSWIKIGVSPVHCITKTVENELPPENIEVSQVQNYVYLKWDYTYANNFTFOVQWLHAF 284  
QY 241 KKNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRQVQSDGNNTSFWSEIEKFTD 300  
DB 285 KKNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRQVQSDGNNTSFWSEIEKFTD 344  
QY 301 EIQAFLLPVPFNIRSLSDSFHYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKII 360

DB 345 EIQAFLLPVPFNIRSLSDSFHYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKII 404  
QY 361 KKTDTVTNPKPLTVYCVKARAHWTDEKLNKSSVFSDAVCE 401  
DB 405 KKTDTVTNPKPLTVYCVKARAHWTDEKLNKSSVFSDAVCE 445

Search completed: January 18, 2006, 06:28:56  
Job time : 80 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:18:53 ; Search time 81.4456 Seconds  
(without alignments)  
2057.195 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKNLKSPQKVEVDIIDNFI.....ARTMDEKLKSSVFSDAVCE 401

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	436	3	US-09-240-675-2
2	2141	100.0	436	4	US-10-824-981-2
3	2141	100.0	436	5	US-10-473-127-1756
4	2141	100.0	436	5	US-10-473-127-1758
5	2141	100.0	436	5	US-10-473-127-1764
6	2141	100.0	557	3	US-09-240-675-4
7	2141	100.0	557	4	US-10-358-228-3
8	2141	100.0	557	5	US-10-473-127-1757
9	2141	100.0	557	5	US-10-473-127-1759
10	2141	100.0	557	5	US-10-473-127-1760
11	2141	100.0	557	5	US-10-473-127-1761
12	2141	100.0	557	5	US-10-473-127-1763
13	2141	100.0	557	5	US-10-473-127-1765
14	2141	100.0	557	5	US-10-473-127-1766
15	2141	100.0	557	5	US-10-473-127-1772
16	2141	100.0	557	5	US-10-473-127-1773
17	2138	99.9	441	5	US-10-764-833-41
18	2137	99.8	557	5	US-10-473-127-1768
19	2136	99.8	434	5	US-10-473-127-1770
20	2136	99.8	557	4	US-10-824-981-4
21	2136	99.8	557	5	US-10-473-127-1769
22	2136	99.8	575	3	US-09-925-300-1672
23	2136	99.8	575	5	US-10-473-127-1762
24	2136	99.8	575	5	US-10-450-763-47653
25	2136	99.8	436	5	US-10-473-127-1767
26	2084	97.3	496	5	US-10-473-127-1771
27	1384.5	64.7	560	4	US-10-293-832-29

28 1377.5 64.3 560 4 US-10-293-832-30 Sequence 30, Appl  
29 488.5 22.8 198 4 US-10-293-832-33 Sequence 33, Appl  
30 228 10.6 273 4 US-10-186-180-13 Sequence 15, Appl  
31 226 10.6 273 4 US-10-186-180-14 Sequence 14, Appl  
32 225 10.5 220 3 US-09-925-055D-19 Sequence 19, Appl  
33 225 10.5 220 4 US-10-807-837-44 Sequence 44, Appl  
34 225 10.5 273 4 US-10-186-180-2 Sequence 2, Appl  
35 225 10.5 273 4 US-10-358-228-8 Sequence 8, Appl  
36 225 10.5 476 3 US-09-925-055D-23 Sequence 23, Appl  
37 225 10.5 476 4 US-10-104-919-62 Sequence 62, Appl  
38 225 10.5 476 5 US-10-395-741B-63 Sequence 63, Appl  
39 225 10.5 476 5 US-10-968-432-62 Sequence 62, Appl  
40 224 10.5 273 4 US-10-186-180-16 Sequence 16, Appl  
41 220 10.3 325 3 US-09-870-574-3 Sequence 3, Appl  
42 220 10.3 325 3 US-09-949-192-5 Sequence 5, Appl  
43 220 10.3 325 4 US-10-052-586-390 Sequence 390, App  
44 220 10.3 325 4 US-10-066-500-137 Sequence 137, App  
45 220 10.3 325 4 US-10-174-590-390 Sequence 390, App

#### ALIGNMENTS

##### RESULT 1

US-09-240-675-2

; Sequence 2, Application US/09240675  
; Patent No. US20020055492A1

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: FLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/240,675

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: PCT/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 17283/117/GUPL

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 436 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-240-675-2

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Query Match      100.0%; Score 2141; DB 3; Length 436;
Best Local Similarity 100.0%; Pred. No. 3e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESQVNTFSDYQKTGMDNWKLSGCGQNTSTK 60
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESQVNTFSDYQKTGMDNWKLSGCGQNTSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIVIHI 120
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIVIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 206

Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVONQYVLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 300
Db 267 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIOQYPLIYIIIFWENTSNAERKIIIE 360
Db 327 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIOQYPLIYIIIFWENTSNAERKIIIE 386

Qy 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 2
US-10-824-981-2
; Sequence 2, Application US/10824981
; Publication No. US20040191840A1
; GENERAL INFORMATION:
; APPLICANT: Benoit, Patrick
; APPLICANT: Maguire, Deborah
; APPLICANT: Plavec, Ivan
; APPLICANT: Tovy, Michael
; APPLICANT: Meyer, Francois
; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With
; FILE REFERENCE: A-7230-2
; CURRENT APPLICATION NUMBER: US/10/824,981
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US 09/240,675
; PRIOR FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: US 08/307,588
; PRIOR FILING DATE: 1994-12-05
; PRIOR APPLICATION NUMBER: PCT/EP93/00770
; PRIOR FILING DATE: 1993-03-30
; PRIOR APPLICATION NUMBER: EP 92400902.0
; PRIOR FILING DATE: 1992-03-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-824-981-2

Query Match      100.0%; Score 2141; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 3e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESQVNTFSDYQKTGMDNWKLSGCGQNTSTK 60
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESQVNTFSDYQKTGMDNWKLSGCGQNTSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIVIHI 120
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIVIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 206

Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVONQYVLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT 300
Db 267 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIOQYPLIYIIIFWENTSNAERKIIIE 360
Db 327 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIOQYPLIYIIIFWENTSNAERKIIIE 386

Qy 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 3
US-10-473-127-1756
; Sequence 1756, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1756
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1756

Query Match      100.0%; Score 2141; DB 5; Length 436;
Best Local Similarity 100.0%; Pred. No. 3e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESQVNTFSDYQKTGMDNWKLSGCGQNTSTK 60
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESQVNTFSDYQKTGMDNWKLSGCGQNTSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIVIHI 120
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIVIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPEPTYICLKVKAAAL 206

Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVONQYVLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSQVONQYVLKWDYTYANMTFQVQWLHAF 266
```

Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVKWDYTYANMTFQVQWLHAPL 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
Qy 301 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKIE 360  
Db 327 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKIE 386  
Qy 361 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

## RESULT 4

US-10-473-127-1758  
; Sequence 1758, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1758  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1758

Query Match 100.0%; Score 2141; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESQNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESQNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPVEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPVEVHLEADKAIVIH 146  
Qy 121 SPGTKDSVWVWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGTKDSVWVWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVKWDYTYANMTFQVQWLHAPL 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVKWDYTYANMTFQVQWLHAPL 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
Qy 301 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKIE 360  
Db 327 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKIE 386

## RESULT 6

US-09-240-675-4  
; Sequence 4, Application US/09240675  
; Patent No. US20020055492A1  
; GENERAL INFORMATION:

Qy 361 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427  
RESULT 5  
US-10-473-127-1764  
; Sequence 1764, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1764  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1764  
Query Match 100.0%; Score 2141; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESQNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESQNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPVEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPVEVHLEADKAIVIH 146  
Qy 121 SPGTKDSVWVWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGTKDSVWVWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVKWDYTYANMTFQVQWLHAPL 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVKWDYTYANMTFQVQWLHAPL 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
Qy 301 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKIE 360  
Db 327 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKIE 386  
Qy 361 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

APPLICANT: BENOIT, Patrick  
APPLICANT: MEYER, Francois  
APPLICANT: MAGUIRE, Deborah  
APPLICANT: PLAVEC, Ivan  
APPLICANT: TOVEY, Michael G.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,675  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-240-675-4

Query Match 100.0%; Score 2141; DB 3; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYOKTGMNDNWKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYOKTGMNDNWKLSGCONITSTK 86

Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIIVHI 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIIVHI 146

Qy 121 SPGTKDSVMWALDGLSTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LSWKIGVSPVHCITKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 240  
Db 207 LSWKIGVSPVHCITKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326

Qy 301 EIQAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVQDYPYIYELIIFWNTSNAERKIIIE 360  
Db 327 EIQAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVQDYPYIYELIIFWNTSNAERKIIIE 386

Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 7  
US-10-358-228-3  
Sequence 3, Application US/10358228  
Publication No. US20030211578A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc. et al.  
TITLE OF INVENTION: Interferon Receptor HKABF92  
FILE REFERENCE: PF465C1  
CURRENT APPLICATION NUMBER: US/10/358,228  
CURRENT FILING DATE: 2003-02-05  
PRIOR APPLICATION NUMBER: 09/453,569  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: 09/326,216  
PRIOR FILING DATE: 1999-06-03  
PRIOR APPLICATION NUMBER: 60/088,185  
PRIOR FILING DATE: 1998-06-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 557  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-358-228-3

Query Match 100.0%; Score 2141; DB 4; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYOKTGMNDNWKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYOKTGMNDNWKLSGCONITSTK 86

Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIIVHI 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEADKAIIVHI 146

Qy 121 SPGTKDSVMWALDGLSTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LSWKIGVSPVHCITKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 240  
Db 207 LSWKIGVSPVHCITKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326

Qy 301 EIQAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVQDYPYIYELIIFWNTSNAERKIIIE 360  
Db 327 EIQAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVQDYPYIYELIIFWNTSNAERKIIIE 386

Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 8  
US-10-473-127-1757  
Sequence 1757, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26

```
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1757
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1759

Query Match      100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFFSDYQKTGMDNWKLSGCCQNTSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFFSDYQKTGMDNWKLSGCCQNTSTK 86
Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNVYKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNVYKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 300
Db 267 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 326
Qy 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKIIIE 360
Db 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKIIIE 386
Qy 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 9
US-10-473-127-1759
; Sequence 1759, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1760
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1760
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; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1759
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1759

Query Match      100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFFSDYQKTGMDNWKLSGCCQNTSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFFSDYQKTGMDNWKLSGCCQNTSTK 86
Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNVYKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNVYKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 300
Db 267 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 326
Qy 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKIIIE 360
Db 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKIIIE 386
Qy 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 10
US-10-473-127-1760
; Sequence 1760, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1760
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1760
```

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDES VGNVTFSDYQKTMNDNWKLSGCGNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDES VGNVTFSDYQKTMNDNWKLSGCGNITSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120  
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy 181 LTSWKIGVYSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 300  
Db 267 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYEEIIFWENTSNAERKII E 360  
Db 327 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYEEIIFWENTSNAERKII E 386

Qy 361 KKTDTVPNLKP LTVYCVKARAHTMDEKLNKSSVFS DAVCE 401  
Db 387 KKTDTVPNLKP LTVYCVKARAHTMDEKLNKSSVFS DAVCE 427

## RESULT 11

US-10-473-127-1761  
; Sequence 1761, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1761  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1761

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDES VGNVTFSDYQKTMNDNWKLSGCGNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDES VGNVTFSDYQKTMNDNWKLSGCGNITSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120

Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180

Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy 181 LTSWKIGVYSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAF 240

Db 207 LTSWKIGVYSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 300

Db 267 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYEEIIFWENTSNAERKII E 360

Db 327 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYEEIIFWENTSNAERKII E 386

Qy 361 KKTDTVPNLKP LTVYCVKARAHTMDEKLNKSSVFS DAVCE 401

Db 387 KKTDTVPNLKP LTVYCVKARAHTMDEKLNKSSVFS DAVCE 427

## RESULT 12

US-10-473-127-1763  
; Sequence 1763, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1763  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1763

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDES VGNVTFSDYQKTMNDNWKLSGCGNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDES VGNVTFSDYQKTMNDNWKLSGCGNITSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120  
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180

Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy 181 LTSWKIGVYSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAF 240

Db 207 LTSWKIGVYSPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFQNGVYKQGIYLLRVOASDGNNTSFWSBEIKEDT 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFQNGVYKQGIYLLRVOASDGNNTSFWSBEIKEDT 326  
Qy 301 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNARKEKIE 360  
Db 327 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNARKEKIE 386  
Qy 361 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 13  
US-10-473-127-1765  
; Sequence 1765, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1765  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1765

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYQKTGMNDWIKLSCQCNITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYQKTGMNDWIKLSCQCNITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIIVHI 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIIVHI 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 206  
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANNMTFQVWLHAPL 240  
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANNMTFQVWLHAPL 266  
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFQNGVYKQGIYLLRVOASDGNNTSFWSBEIKEDT 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFQNGVYKQGIYLLRVOASDGNNTSFWSBEIKEDT 326  
Qy 301 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNARKEKIE 360  
Db 327 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNARKEKIE 386  
Qy 361 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

Db 387 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 14  
US-10-473-127-1766  
; Sequence 1766, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1766  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1766

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYQKTGMNDWIKLSCQCNITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYQKTGMNDWIKLSCQCNITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIIVHI 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIIVHI 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 206  
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANNMTFQVWLHAPL 240  
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANNMTFQVWLHAPL 266  
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFQNGVYKQGIYLLRVOASDGNNTSFWSBEIKEDT 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFQNGVYKQGIYLLRVOASDGNNTSFWSBEIKEDT 326  
Qy 301 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNARKEKIE 360  
Db 327 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWENTSNARKEKIE 386  
Qy 361 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNPKLPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 15  
US-10-473-127-1772  
; Sequence 1772, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING



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; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1772
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1772

Query Match      100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. NO. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GKNLKSQKVEVDIIDNFIILNRNRSDESGVNTFFSDYQKTGMNDNWKLSGCONITSTK 60
Db      27  GKNLKSQKVEVDIIDNFIILNRNRSDESGVNTFFSDYQKTGMNDNWKLSGCONITSTK 86

Qy      61  CNFSSLKLNYYEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIHI 120
Db      87  CNFSSLKLNYYEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIHI 146

Qy     121  SPGTKDSVMALDGLSTYSLLIWNSSGVEERENIYSRHKIYKLSPETTYCLKVKAAL 180
Db     147  SPGTKDSVMALDGLSTYSLLIWNSSGVEERENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy     181  LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNVKWDVTYANMTFQVQWLHAF 240
Db     207  LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNVKWDVTYANMTFQVQWLHAF 266

Qy     241  KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db     267  KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326

Qy     301  EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYBIIIFWNTSNAERKIE 360
Db     327  EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYBIIIFWNTSNAERKIE 386

Qy     361  KKTDTVTPLKPLTVYCVKARAHTMDKLNKSSVFSDAVCE 401
Db     387  KKTDTVTPLKPLTVYCVKARAHTMDKLNKSSVFSDAVCE 427
```

Search completed: January 17, 2006, 07:35:30  
Job time : 82.4456 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 07:19:53 ; Search time 16.2891 Seconds  
(without alignments)  
232.741 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKNIKSPQKVEVDIIDNFI.....AHTWDEKLNKSSVFSFSDAVCE 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pdb.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pdb.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pdb.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pdb.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US03\_NEW\_PUB.pdb.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pdb.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pdb.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	8.5	542	6 US-10-131-826A-188	Sequence 188, Appl
2	180	8.4	553	6 US-10-636-716-2	Sequence 2, Appli
3	180	8.4	553	6 US-10-636-716-14	Sequence 14, Appl
4	180	8.4	553	6 US-10-636-716-16	Sequence 16, Appl
5	180	8.4	553	6 US-10-636-716-18	Sequence 18, Appl
6	180	8.4	553	6 US-10-636-716-20	Sequence 20, Appl
7	180	8.4	553	6 US-10-636-716-22	Sequence 22, Appl
8	180	8.4	553	6 US-10-636-716-24	Sequence 24, Appl
9	180	8.4	553	6 US-10-636-716-26	Sequence 26, Appl
10	180	8.4	553	6 US-10-636-716-28	Sequence 28, Appl
11	180	8.4	553	6 US-10-636-716-30	Sequence 30, Appl
12	180	8.4	553	6 US-10-636-716-32	Sequence 32, Appl
13	180	8.4	553	6 US-10-636-716-34	Sequence 34, Appl
14	180	8.4	553	6 US-10-636-716-36	Sequence 36, Appl
15	180	8.4	553	6 US-10-636-716-38	Sequence 38, Appl
16	180	8.4	553	6 US-10-636-716-40	Sequence 40, Appl
17	180	8.4	553	6 US-10-636-716-42	Sequence 42, Appl
18	180	8.4	553	6 US-10-636-716-44	Sequence 44, Appl
19	180	8.4	553	6 US-10-636-716-46	Sequence 46, Appl
20	180	8.4	553	6 US-10-636-716-48	Sequence 48, Appl
21	172.5	8.1	221	6 US-10-636-716-56	Sequence 56, Appl
22	167.5	7.8	221	6 US-10-636-716-54	Sequence 54, Appl
23	166.5	7.8	221	6 US-10-636-716-50	Sequence 50, Appl
24	166.5	7.8	384	7 US-11-075-351-12	Sequence 12, Appl
25	166.5	7.8	404	7 US-11-075-351-23	Sequence 23, Appl

26	166.5	7.8	404	7 US-11-075-351-25	Sequence 25, Appl
27	165.5	7.7	221	6 US-10-636-716-52	Sequence 52, Appl
28	163.5	7.6	221	6 US-10-636-716-60	Sequence 60, Appl
29	160.5	7.5	221	6 US-10-636-716-58	Sequence 58, Appl
30	147.5	6.9	311	6 US-10-131-826A-32	Sequence 32, Appl
31	147.5	6.9	311	6 US-10-512-214-16	Sequence 16, Appl
32	147.5	6.9	366	7 US-11-075-351-38	Sequence 38, Appl
33	147.5	6.9	374	7 US-11-075-351-42	Sequence 42, Appl
34	142	6.6	574	7 US-11-102-240-164	Sequence 164, App
35	123	5.7	522	7 US-11-184-399-8	Sequence 8, Appli
36	118	5.5	1005	7 US-11-113-424-63	Sequence 63, Appl
37	117.5	5.5	2214	7 US-11-080-991-94	Sequence 94, Appl
38	115	5.4	244	7 US-11-184-399-10	Sequence 10, Appl
39	115	5.4	473	7 US-11-165-141-23	Sequence 23, Appl
40	115	5.4	520	7 US-11-098-662-12	Sequence 12, Appl
41	115	5.4	520	7 US-11-165-141-19	Sequence 19, Appl
42	115	5.4	599	7 US-11-165-141-33	Sequence 33, Appl
43	109	5.1	203	7 US-11-165-141-4	Sequence 4, Appli
44	109	5.1	491	7 US-11-098-662-14	Sequence 14, Appl
45	109	5.1	491	7 US-11-165-141-2	Sequence 2, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-131-826A-188  
; Sequence 188, Application US/10131826A  
; Publication No. US20050245730A1

#### GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128

; CURRENT APPLICATION NUMBER: US/10/131,826A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

```
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 188
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-188

Query Match      8.5%; Score 182; DB 6; Length 542;
Best Local Similarity 20.6%; Pred. No. 1.8e-08;
Matches 85; Conservative 76; Mismatches 165; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDNFILRNWRSDESVG-VNTFSFDYQKTGMNDWIKLSGCONITSTKCN 62
Db 26 LPKPNITFLSINMKNVLQWTPPEGLOGVKVYTYVQYFIYQKKWLKSECRNINRTYCD 85
Qy 63 FSSLKLVYBEIKLIRA-EKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHIS 121
Db 86 LSAETSDYEHQYAKVKAINGTKSKWAESGRFPFLETQIGPPEVALTTDEKSISVLT 145
Qy 122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIENIYSRHKIYK--LSPET 170
Db 146 APEKWKRNPELPSVMQIYSLNLYNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 201
Qy 171 TYCLKVKAALTSWKIGVSPVHCITKTVENE-----LPPENIEVSQVQNY 218
Db 202 LYCVHVESFVPGPRRAQPSKQCARLTKQOSSEFKAKIIFWYVLP-----ISITV----- 252
Qy 219 VLKWDYTYANMTFQV-QWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQGIY 277
Db 253 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNFDRKFF 290
Qy 278 LLRVQASDGNNTSFWSBEIKEDTEI---QAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 334
Db 291 V-----PAEKIVINFTLNISDSSKISHQDMSLLGKSSDVSSLND-----POPSGNLR 338
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIEKKTVDV--TVPNLKPLTVY 376
Db 339 PQQEEEVKHLGYASHLMEIFCDSEENTEGTSLTQBSLSRTIPDPKTVIEY 390

RESULT 2
US-10-636-716-2
; Sequence 2, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 188
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-188

PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-2

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDNFILRNWRSDESVG-VNTFSFDYQKTGMNDWIKLSGCONITSTKCN 62
Db 37 LPKPNITFLSINMKNVLQWTPPEGLOGVKVYTYVQYFIYQKKWLKSECRNINRTYCD 96
Qy 63 FSSLKLVYBEIKLIRA-EKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHIS 121
Db 97 LSAETSDYEHQYAKVKAINGTKSKWAESGRFPFLETQIGPPEVALTTDEKSISVLT 156
Qy 122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIENIYSRHKIYK--LSPET 170
Db 157 APEKWKRNPELPSVMQIYSLNLYNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212
Qy 171 TYCLKVKAALTSWKIGVSPVHCITKTVENE-----LPPENIEVSQVQNY 218
Db 213 LYCVHVESFVPGPRRAQPSKQCARLTKQOSSEFKAKIIFWYVLP-----ISITV----- 263
Qy 219 VLKWDYTYANMTFQV-QWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQGIY 277
Db 264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNFDRKFF 301
Qy 278 LLRVQASDGNNTSFWSBEIKEDTEI---QAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 334
Db 302 V-----PAEKIVINFTLNISDSSKISHQDMSLLGKSSDVSSLND-----POPSGNLR 349
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIEKKTVDV--TVPNLKPLTVY 376
Db 350 PQQEEEVKHLGYASHLMEIFCDSEENTEGTSLTQBSLSRTIPDPKTVIEY 401

RESULT 3
US-10-636-716-14
; Sequence 14, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
```

ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lund, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-14

Query Match 8.4%; Score 180; DB 6; Length 553;

Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIDNFIILRNRSDESVG-NVTFSPDYQKTGMNWKLSGQCNITSTKCN 62  
Db 37 LPKPANITFLSINMKNVLQWTPPEGLQGVKTYTVQYFIYQKKWLKSECRNIRTYCD 96  
Qy 63 FSSILKLVYERIKLIRA-EKENTSSWYEVDSFTPFRAQIGPPPEVHLEAEDKAIVHIS 121  
Db 97 LSATSDYEHQYAKVKAIGTKCKWAESGRFPFLETQIGPPEVALTTDEKSI SVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLLIWKSSGVEERIENIYSRHKIYK--LSPET 170  
Db 157 APEKWRNPEDLPVSMQOIYSLNLYNVSIVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAALTSWKIGYSPVHCIKTTVENE-----LPPPENIEVSQNY 218  
Db 213 LYCHVESFVGPFPRAQPSKQCAKTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTFOV-OWLHAFLEKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDKRF 301  
Qy 278 LLRVOASGNNTSFWSEIKFDTEI---QAFLLPVFNIRSLDSFHYIYIAPKQSGNTP 334  
Db 302 V-----PAEKIVNFTILNIDSDSKISHQMSLLGKSDVSLND-----POPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWNTSNAERKIEKKTIV--TVPNLKLPTVY 376  
Db 350 PPQEEEVKHLGYASHLMEIFCDSENTGTSFTQOESLSRTIPDPKTVIEY 401

RESULT 4

US-10-636-716-16  
; Sequence 16, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:

APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Fairah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lund, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-16

Query Match 8.4%; Score 180; DB 6; Length 553;

Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIDNFIILRNRSDESVG-NVTFSPDYQKTGMNWKLSGQCNITSTKCN 62  
Db 37 LPKPANITFLSINMKNVLQWTPPEGLQGVKTYTVQYFIYQKKWLKSECRNIRTYCD 96  
Qy 63 FSSILKLVYERIKLIRA-EKENTSSWYEVDSFTPFRAQIGPPPEVHLEAEDKAIVHIS 121  
Db 97 LSATSDYEHQYAKVKAIGTKCKWAESGRFPFLETQIGPPEVALTTDEKSI SVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLLIWKSSGVEERIENIYSRHKIYK--LSPET 170  
Db 157 APEKWRNPEDLPVSMQOIYSLNLYNVSIVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAALTSWKIGYSPVHCIKTTVENE-----LPPPENIEVSQNY 218  
Db 213 LYCHVESFVGPFPRAQPSKQCAKTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTFOV-OWLHAFLEKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDKRF 301

Qy 278 LLRQASDGNNTSFWSEIEKFDTEI---QAPLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 334  
Db 302 V-----PAEKIVINFITLINSDDSKISHQMSLLGKSSDVSSLND-----PQPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTDV--TVPNLKLPLTVY 376  
Db 350 PQOESEVKHLGYASHLMEIFCDSEENTGTSFTQOESLSRTIPPDKTVIEY 401

RESULT 5  
US-10-636-716-18  
; Sequence 18, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-10-636-716-18

Query Match 8.4%; Score 180; DB 6; Length 553;  
Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDNFIILRNRSDESVG-NVTFSDYQKTGMNDWIKLSCQNTITKCN 62  
Db 37 LKPEANITFLSINKNVQLQWTFPPGLQGVKVTYVQYFIYGKQKLNKSCRINRTYCD 96  
Qy 63 FSLKLVNVEIKRIRA-EKENTSSWYVDSTFPFRKAQIGPPVHLEADKAIVTHIS 121

Db 97 LSAETSDYEHQYAKVKAIMGTKCSKWAESGREYFPLETQIGPPEVALTTDEKSIYVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLLIWKNSGSGVEERIEIYSRHKIYK--LSPET 170  
Db 157 APKWRKNPEDLPVSMQIYSNLUKNVSLNTKSNRTWSOCVTN-----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAALLTSWKIGVYSPVHCITVTENE-----LPPPENIEVSVQONQY 218  
Db 213 LYCVHVESFVPGPPRAQPSKQCAKTLKQSSSEPKAKIIFWVYLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTQV--QWLHAFILKRNPNHLYKWKQIPDCENVKTTCQVFPQNVFQGIY 277  
Db 264 -----FLFSVMGYSIYRIYHVGEKEHPANLI-----LIYGNFEFKRFF 301  
Qy 278 LLRQASDGNNTSFWSEIEKFDTEI---QAPLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 334  
Db 302 V-----PAEKIVINFITLINSDDSKISHQMSLLGKSSDVSSLND-----PQPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTDV--TVPNLKLPLTVY 376  
Db 350 PQOESEVKHLGYASHLMEIFCDSEENTGTSFTQOESLSRTIPPDKTVIEY 401

RESULT 6  
US-10-636-716-20  
; Sequence 20, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-22

Query Match  
Best Local Similarity 8.4%; Score 180; DB 6; Length 553;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSDFYQKTMGNWIKLSCQNITTKCN 62  
37 LPKANITFLSINKNVLTQTPPEGLQGVKVTYVQYFIYGQKKWLNKSECRINRTYCD 96  
63 FSSKLNVYEIKLIRA-EKENTSSWYVDSTFPRKAOIGPEVHLEADKAIVHIS 121  
97 LSAETSDYEHQYAKVAIWGTCCKWAESGRFPFLETQIGPEVALTTDEKSISVLT 156  
122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIENIYSRHKIYK--LSPET 170  
157 APEKWRNPEDLPVSMQIYSLNKNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
171 TYCLVKVKAALTSWKIGYSPVHCIKTTVENE-----LPPENIEVSQVQNY 218  
213 LYCVHVESFVPGPRRAQSEKQKARTLKQSSSEFKAKIIFWVLP-----ISITV----- 263  
219 VLKWDYTYANMTFQV-QWLHAFILRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277  
264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNEFDKRRF 301  
278 LLRQVQSGNNTSFWSEBEIKFDTEI---QAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 334  
302 V-----PAEKIVINFITLISDSSKISHQDMSLLGKSSDVSLND-----POPSGNLR 349  
335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD--TVPNLKPLTVY 376  
350 PQEVEEVKHLGYASHLMEIFCDSEENTGTSFTQQESLSRTIPDKTIVIEY 401

RESULT 8  
US-10-636-716-24  
Sequence 24, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-Seq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997

MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-20

Query Match  
Best Local Similarity 8.4%; Score 180; DB 6; Length 553;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSDFYQKTMGNWIKLSCQNITTKCN 62  
37 LPKANITFLSINKNVLTQTPPEGLQGVKVTYVQYFIYGQKKWLNKSECRINRTYCD 96  
63 FSSKLNVYEIKLIRA-EKENTSSWYVDSTFPRKAOIGPEVHLEADKAIVHIS 121  
97 LSAETSDYEHQYAKVAIWGTCCKWAESGRFPFLETQIGPEVALTTDEKSISVLT 156  
122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIENIYSRHKIYK--LSPET 170  
157 APEKWRNPEDLPVSMQIYSLNKNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
171 TYCLVKVKAALTSWKIGYSPVHCIKTTVENE-----LPPENIEVSQVQNY 218  
213 LYCVHVESFVPGPRRAQSEKQKARTLKQSSSEFKAKIIFWVLP-----ISITV----- 263  
219 VLKWDYTYANMTFQV-QWLHAFILRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277  
264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNEFDKRRF 301  
278 LLRQVQSGNNTSFWSEBEIKFDTEI---QAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 334  
302 V-----PAEKIVINFITLISDSSKISHQDMSLLGKSSDVSLND-----POPSGNLR 349  
335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD--TVPNLKPLTVY 376  
350 PQEVEEVKHLGYASHLMEIFCDSEENTGTSFTQQESLSRTIPDKTIVIEY 401

RESULT 7  
US-10-636-716-22  
Sequence 22, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-Seq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-22

Query Match  
Best Local Similarity 8.4%; Score 180; DB 6; Length 553;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSDFYQKTMGNWIKLSCQNITTKCN 62  
37 LPKANITFLSINKNVLTQTPPEGLQGVKVTYVQYFIYGQKKWLNKSECRINRTYCD 96  
63 FSSKLNVYEIKLIRA-EKENTSSWYVDSTFPRKAOIGPEVHLEADKAIVHIS 121  
97 LSAETSDYEHQYAKVAIWGTCCKWAESGRFPFLETQIGPEVALTTDEKSISVLT 156  
122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIENIYSRHKIYK--LSPET 170  
157 APEKWRNPEDLPVSMQIYSLNKNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
171 TYCLVKVKAALTSWKIGYSPVHCIKTTVENE-----LPPENIEVSQVQNY 218  
213 LYCVHVESFVPGPRRAQSEKQKARTLKQSSSEFKAKIIFWVLP-----ISITV----- 263  
219 VLKWDYTYANMTFQV-QWLHAFILRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277  
264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNEFDKRRF 301  
278 LLRQVQSGNNTSFWSEBEIKFDTEI---QAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 334  
302 V-----PAEKIVINFITLISDSSKISHQDMSLLGKSSDVSLND-----POPSGNLR 349  
335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD--TVPNLKPLTVY 376  
350 PQEVEEVKHLGYASHLMEIFCDSEENTGTSFTQQESLSRTIPDKTIVIEY 401

RESULT 8  
US-10-636-716-24  
Sequence 24, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-Seq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997

MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-20

Query Match  
Best Local Similarity 8.4%; Score 180; DB 6; Length 553;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSDFYQKTMGNWIKLSCQNITTKCN 62  
37 LPKANITFLSINKNVLTQTPPEGLQGVKVTYVQYFIYGQKKWLNKSECRINRTYCD 96  
63 FSSKLNVYEIKLIRA-EKENTSSWYVDSTFPRKAOIGPEVHLEADKAIVHIS 121  
97 LSAETSDYEHQYAKVAIWGTCCKWAESGRFPFLETQIGPEVALTTDEKSISVLT 156  
122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIENIYSRHKIYK--LSPET 170  
157 APEKWRNPEDLPVSMQIYSLNKNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
171 TYCLVKVKAALTSWKIGYSPVHCIKTTVENE-----LPPENIEVSQVQNY 218  
213 LYCVHVESFVPGPRRAQSEKQKARTLKQSSSEFKAKIIFWVLP-----ISITV----- 263  
219 VLKWDYTYANMTFQV-QWLHAFILRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277  
264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNEFDKRRF 301  
278 LLRQVQSGNNTSFWSEBEIKFDTEI---QAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 334  
302 V-----PAEKIVINFITLISDSSKISHQDMSLLGKSSDVSLND-----POPSGNLR 349  
335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD--TVPNLKPLTVY 376  
350 PQEVEEVKHLGYASHLMEIFCDSEENTGTSFTQQESLSRTIPDKTIVIEY 401

RESULT 7  
US-10-636-716-22  
Sequence 22, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-Seq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-24

Query Match 8.4%; Score 180; DB 6; Length 553;

Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDDNFILNRNRSDESVG-NVTFSDYQKTMGMNWKLSGQNITSTKCN 62  
Db 37 LPKPANITFLSINKMKNVLTQTPPEGLQGVKVTYTVQYFIYQKKWLNKSECRNINRTYCD 96  
Qy 63 FSSKLNVYEIKLRIRA-EKENTSSWYEVDSFTFPRKAIQGPPEVHLEADKAIVIHIS 121  
Db 97 LSAETSDYEHQYAKVKAIWGTCSCWAESGRFPFLEQTIGPPEVALTTDEKSI SVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYK--LSPET 170  
Db 157 APEKWKRNPELPSVMQIYSLNKNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAAALTSWKIGYSPVHCITTVENE-----LPPENIEVSQONQY 218  
Db 213 LYCVHVESFVPGPPRAQPSKQCARTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTFQV-QWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNFEDKRF 301  
Qy 278 LLRVOASDGNNTFSWSEIEKFDTEI---QAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334  
Db 302 V-----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLND-----PPSGNLR 349  
Qy 335 VIQDYPIIYEI-----IFWENTSNAERKIIIEKKTDTV--TVPNLKLPTVY 376  
Db 350 PPOEEEVHGLGYASHLMEIFCDSEENTEGTSFTQOESLSRTIIPDKTIVIEY 401

## RESULT 9

US-10-636-716-26  
Sequence 26, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmborg, Anna C.

APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-26

Query Match 8.4%; Score 180; DB 6; Length 553;

Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDDNFILNRNRSDESVG-NVTFSDYQKTMGMNWKLSGQNITSTKCN 62  
Db 37 LPKPANITFLSINKMKNVLTQTPPEGLQGVKVTYTVQYFIYQKKWLNKSECRNINRTYCD 96  
Qy 63 FSSKLNVYEIKLRIRA-EKENTSSWYEVDSFTFPRKAIQGPPEVHLEADKAIVIHIS 121  
Db 97 LSAETSDYEHQYAKVKAIWGTCSCWAESGRFPFLEQTIGPPEVALTTDEKSI SVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLIWKNSGVEERIENIYSRHKIYK--LSPET 170  
Db 157 APEKWKRNPELPSVMQIYSLNKNVSVLTKSNRTWSQCVTN-----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAAALTSWKIGYSPVHCITTVENE-----LPPENIEVSQONQY 218  
Db 213 LYCVHVESFVPGPPRAQPSKQCARTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTFQV-QWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRIYHVGEKHPANLI-----LIYGNFEDKRF 301  
Qy 278 LLRVOASDGNNTFSWSEIEKFDTEI---QAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334  
Db 302 V-----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLND-----PPSGNLR 349



```
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIEKKTIV--TVPNLKPLTVY 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 350 PQEEREVKHGYASHLMELFCDSSENTGTSFTQESLSRTIPPDKTIVIEY 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-636-716-28
; Sequence 28, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-28

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIDNFIILWRNRSDEVG-VNTPFSFDYQKTMGMDWIKLSCGNITSTKCN 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 37 LPKPNITFLSINMKNVLQWTPPEGLQGVKVTYTVYFYIGQKWLNFSECRNINRTYCD 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 63 FSSLNLYVEELKLRIR-ERKENTSSWYEVDSFTFPRKAQIGPPEVHLEAEDKAIVIHIS 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 LSAETSDYEHQYAKVAINGTKCSKWAESGRFPFLETQIGPPEVALTTDEKSLSVVLT 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 122 PGTK-----DSVMWALDGLSFTYSLIIWKNSSGVBERIENIYSRHKIYK--LSPET 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 157 APEKWRNPEDLPVSMQOIYSNLKYNVSLNTKSNRTWSQCVTN-----HTLVLTWLSBENT 212
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 171 TYCLKVKAAALLTSWKIGVYSPVHCICKTTVENE-----LPPPENIEVSVQNOQNY 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 LYCVHVESFVGPGRRAQPSKQCARLKDQSSSEFKAKIIFWYVLP-----ISITV----- 263
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 219 VLKWDYTYANMTFQV-QWLHAFILKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 264 -----PLFSVMGYSIYRIHVHGKEKHPANLI-----LIYGNFEFKRFF 301
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 278 LLRVQASDGNNTSFWSEEIKFDEI-----QAFLLPPVENIRSLSDSFHYIYGAPKQSGNTP 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 V-----PAEKIVINFITLNISSDKISHQDMSLLGKSSDVSVSLND-----POPSGNLR 349
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIEKKTIV--TVPNLKPLTVY 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 350 PQEEREVKHGYASHLMELFCDSSENTGTSFTQESLSRTIPPDKTIVIEY 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-30
```

Query Match 8.4%; Score 180; DB 6; Length 553;  
Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSFDYQKTMNDWIKLSCQNTITSTKCN 62  
Db 37 LPKPANITFLSINMKVQLWTPPEGLOGVKVYTYVQYFIYGKKWLNKSECRNINRTYCD 96  
Qy 63 FSSKLNVYEIKLRIRA-EKENTSSWYEVDSPTFRKAQIGPPEVHLEAEDKAIVHIS 121  
Db 97 LSAETSDYEHQYAKVAIWGTRKSKWABSGRFYFLETQIGPPEVALTTDEKSISVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIEINIYSRHKIYK--LSPET 170  
Db 157 APEKWKRNPEDLPSVMQOIYSLNKNVSVLTKNSRTWSQCVTN----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAAALTSWKIGVSPVHCITVTENE-----LPPENIEVSQVQNY 218  
Db 213 LYCVHVESFVGPRAQPSKOCARTLKQOSSEFKAKIIFWYVLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTFQV-OWLHAFKRNPNHLYKWKQIPDCENVKTTQCVPPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNFDRFF 301  
Qy 278 LLRVQASDGNNTSFWSBEEKPDTEI---QAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 334  
Db 302 V----PAEKIVNIFITLNISSDKISHQMSLLGKSSDVSSLND-----PQPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWNTSNAERKIEKKTDV--TVPNLKLPTVY 376  
Db 350 PQESEEVKHLGYASHLMELFCDSEENTGTSFTQESLSRTIPPDKTVIEY 401

RESULT 12

US-10-636-716-32  
; Sequence 32, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmeberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-10-636-716-32

Query Match 8.4%; Score 180; DB 6; Length 553;

Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSFDYQKTMNDWIKLSCQNTITSTKCN 62  
Db 37 LPKPANITFLSINMKVQLWTPPEGLOGVKVYTYVQYFIYGKKWLNKSECRNINRTYCD 96  
Qy 63 FSSKLNVYEIKLRIRA-EKENTSSWYEVDSPTFRKAQIGPPEVHLEAEDKAIVHIS 121  
Db 97 LSAETSDYEHQYAKVAIWGTRKSKWABSGRFYFLETQIGPPEVALTTDEKSISVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLIWNKSSGVEERIEINIYSRHKIYK--LSPET 170  
Db 157 APEKWKRNPEDLPSVMQOIYSLNKNVSVLTKNSRTWSQCVTN----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAAALTSWKIGVSPVHCITVTENE-----LPPENIEVSQVQNY 218  
Db 213 LYCVHVESFVGPRAQPSKOCARTLKQOSSEFKAKIIFWYVLP-----ISITV----- 263  
Qy 219 VLKWDYTYANMTFQV-OWLHAFKRNPNHLYKWKQIPDCENVKTTQCVPPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNFDRFF 301  
Qy 278 LLRVQASDGNNTSFWSBEEKPDTEI---QAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 334  
Db 302 V----PAEKIVNIFITLNISSDKISHQMSLLGKSSDVSSLND-----PQPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWNTSNAERKIEKKTDV--TVPNLKLPTVY 376  
Db 350 PQESEEVKHLGYASHLMELFCDSEENTGTSFTQESLSRTIPPDKTVIEY 401

RESULT 13

US-10-636-716-34  
; Sequence 34, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmeberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-34

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy      4 LKSPQKVEVDIIDDNFILRWNRSDSVG-NVTFSPDYQKTCMDNWIKLGGCQNTSTKCN 62
Db      37 LPKPNITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKSECRNIRTYCD 96
Qy      63 FSSLKLANVYBEIKLIRA-EKENTSSWYEVDSFTFPRKQAIGPPPEVHLEADKAIIVHIS 121
Db      97 LSAETSDYEHQYAKVKAIGWTKCSKWAESGRFPFLEQTQIGPPEVALTTDEKSI SVLT 156
Qy      122 PGTK-----DSVMALDGLSTYSLLIWNKSSGVEERIENIYSHKLYK--LSPET 170
Db      157 APERKWRNPEDLPVSMQOIYSLNLYNVSNTKSNRTWSQCVTN-----HTLVLTWLEPNT 212
Qy      171 TYCLKVKAALLTSWKIGYSPVHCITKTVE-----LPPPENIEVSQNYQ 218
Db      213 LYCVHVESFVCPPPRAQPSKQARTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263
Qy      219 VLKWDYTYANMTFOV-QWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
Db      264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDPKRFF 301
Qy      278 LLRVQASDGNNTSFWSEIEKDTETI---QAFLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 334
Db      302 V-----PAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLND-----POPSGNLR 349
Qy      335 VIQDYPLIYEI-----IFWENTSNAERKIEKTDV--TVPNLKPLTVY 376
Db      350 PPQEEVEKHLYGASHLMELFCDSENTGTSFTQOESLSRTIIPDKTVIEY 401

RESULT 14
US-10-636-716-36
; Sequence 36, Application US/10636716
; Publication No. US2005024832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
```

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; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-36

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy      4 LKSPQKVEVDIIDDNFILRWNRSDSVG-NVTFSPDYQKTCMDNWIKLGGCQNTSTKCN 62
Db      37 LPKPNITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKSECRNIRTYCD 96
Qy      63 FSSLKLANVYBEIKLIRA-EKENTSSWYEVDSFTFPRKQAIGPPPEVHLEADKAIIVHIS 121
Db      97 LSAETSDYEHQYAKVKAIGWTKCSKWAESGRFPFLEQTQIGPPEVALTTDEKSI SVLT 156
Qy      122 PGTK-----DSVMALDGLSTYSLLIWNKSSGVEERIENIYSHKLYK--LSPET 170
Db      157 APERKWRNPEDLPVSMQOIYSLNLYNVSNTKSNRTWSQCVTN-----HTLVLTWLEPNT 212
Qy      171 TYCLKVKAALLTSWKIGYSPVHCITKTVE-----LPPPENIEVSQNYQ 218
Db      213 LYCVHVESFVCPPPRAQPSKQARTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263
Qy      219 VLKWDYTYANMTFOV-QWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
Db      264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDPKRFF 301
Qy      278 LLRVQASDGNNTSFWSEIEKDTETI---QAFLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 334
Db      302 V-----PAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSLND-----POPSGNLR 349
Qy      335 VIQDYPLIYEI-----IFWENTSNAERKIEKTDV--TVPNLKPLTVY 376
Db      350 PPQEEVEKHLYGASHLMELFCDSENTGTSFTQOESLSRTIIPDKTVIEY 401
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Db 350 PPOEEEVKHLGYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIEY 401

RESULT 15

US-10-636-716-38  
; Sequence 38, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lund, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal

Query Match 8.4%; Score 180; DB 6; Length 553;  
Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;  
  
Qy 4 LKSPQKVEVDIIDNFIILRNRSDESG-NVTFESFDYQKGMNWKLSGCONITSTKCN 62  
Db 37 LPKPANITFISINWKNVLQWTPPPGLQGVKVTYTVQFIYQKKWLNKSECRNINRYCD 96  
  
Qy 63 FSSLKLVNVEIKLIRIRA-EKENTSSWYEDSFTFPRKAQIGPPPEVHLEAEDKAIVIHIS 121  
Db 97 LSAETSDYEHQYAKVAIKWGTCKWAESGRFYFPLETQIGPPEVALTTDEKSISVULT 156  
  
Qy 122 PGTK-----DSVMWALDGLSFTYSLLIWKNSGVVEERIENIYSRHKYK--LSPET 170  
Db 157 APEKWRKNRPDLVPVSMQOIYSNLKYNVSLNLTGKSNRTWSQCVTN----HTLVLTWLEPNT 212

Qy 171 TYCLKVKAAALLTSWKIGVYSPVHCIIKTTVENE-----LPPPENIEVSQVQNY 218  
Db 213 LYCVHVESFVPGPPRAQSEKQCARLKDQSSSEFKAKIIFWYVLP-----ISITV----- 263  
  
Qy 219 VLKWDYTYANMTQV-QWLHAFILKRNPNHLYKWKQIIPDCENVKTTQCVFPQNVFKGIY 277  
Db 264 -----FLFSVMGYSIYRYIHVGKEKHPANLI-----LIYGNEFDKRRFF 301  
  
Qy 278 LLRVQASDGNNTSFWSSEIKFDTEI---QAFLLPPVPNIBSLSDSFHYIYGAPKQSGNTP 334  
Db 302 V-----PAEKIVINFITLINISDDSKISHQMSLLIGKSDVSSLND-----POPSGNLR 349  
  
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTDV--TVPNLKPLTVY 376  
Db 350 PPOEEEVKHLGYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIEY 401

Search completed: January 17, 2006, 07:36:15  
Job time : 17.2891 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 07:06:01 ; Search time 121.892 Seconds  
(without alignments)  
2523.620 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVVLGATTLVLVAVGPVW.....KSSVFSDAVCEKTKPGNTSK 436

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2307	99.7	557	1 INARI_HUMAN	P17181 homo sapien
2	2307	99.7	557	2 Q53H11_HUMAN	Q53H11 homo sapien
3	2300	99.4	557	2 Q53GW9_HUMAN	Q53GW9 homo sapien
4	2030	87.8	387	2 Q5PKD7_HUMAN	Q5PKD7 homo sapien
5	1699.5	73.5	477	2 Q4R727_MACFA	Q4R727 macaca fasc
6	1546	66.8	560	1 INARI_PIG	Q764M8 sus scrofa
7	1507	65.2	560	1 INARI_BOVIN	Q04790 bos taurus
8	1503	65.0	560	1 INARI_SHEEP	Q28589 ovis aries
9	1154.5	49.9	332	2 Q5GK86_SHEEP	Q5GK86 ovis aries
10	1069	46.2	590	1 INARI_MOUSE	P33896 mus musculus
11	1062	45.9	590	2 Q80UR8_MOUSE	Q80UR8 mus musculus
12	1061	45.9	590	2 Q80UJ3_MOUSE	Q80UJ3 mus musculus
13	695.5	30.1	449	2 Q5XY05_CHICK	Q5XY05 gallus gall
14	695.5	30.1	569	2 Q5XPI1_CHICK	Q5XPI1 gallus gall
15	689.5	29.8	442	2 Q5PVJ9_CHICK	Q5PVJ9 gallus gall
16	686.5	29.7	569	2 Q5YHW0_CHICK	Q5YHW0 gallus gall
17	262.5	11.3	111	2 Q6LDD2_MOUSE	Q6LDD2 mus musculus
18	246	10.6	98	2 Q5LDC2_MOUSE	Q5LDC2 mus musculus
19	232	10.0	317	2 Q88CP3_BOVIN	Q88CP3 bos taurus
20	228.5	9.9	325	2 Q08334_HUMAN	Q08334 homo sapien
21	222.5	9.6	327	2 Q6ZVU9_HUMAN	Q6ZVU9 homo sapien
22	222.5	9.6	349	1 I10R2_MOUSE	Q61190 mus musculus
23	222.5	9.6	351	2 Q8VHM7_MOUSE	Q8VHM7 mus musculus
24	208.5	9.0	362	2 Q764M7_PIG	Q764M7 sus scrofa
25	204.5	8.8	334	2 Q5RL90_CHICK	Q5RL90 gallus gall
26	203	8.8	332	2 Q78EC1_MURRI	Q78EC1 mus sp. int
27	203	8.8	332	2 Q63953_MOUSE	Q63953 mus musculus
28	198	8.6	333	2 Q7ZT30_TETNG	Q7ZT30 tetraodon n
29	198	8.6	553	1 I20RA_HUMAN	Q9UHF4 homo sapien
30	190	8.2	59	2 Q5GK85_SHEEP	Q5GK85 ovis aries
31	189.5	8.2	341	2 Q5YGC8_CHICK	Q5YGC8 gallus gall

32	189	8.2	213	2	Q8C352_MOUSE	Q8C352 mus musculus
33	185.5	8.0	546	1	I20RA_MOUSE	Q6PHB0 mus musculus
34	174	7.5	209	2	Q96SH7_HUMAN	Q96SH7 homo sapien
35	161	7.0	499	2	Q5PPL9_XENLA	Q5PPL9 xenopus lae
36	160.5	6.9	336	2	Q800E8_TETNG	Q800E8 tetraodon n
37	160.5	6.9	502	2	Q5U488_XENLA	Q5U488 xenopus lae
38	155.5	6.7	337	1	INGR2_HUMAN	P38484 homo sapien
39	155.5	6.7	568	2	Q800F7_TETNG	Q800F7 tetraodon n
40	155.5	6.7	568	2	Q800G1_TETNG	Q800G1 tetraodon n
41	153.5	6.6	338	2	Q800G2_TETNG	Q800G2 tetraodon n
42	151	6.5	574	2	Q9HB22_HUMAN	Q9HB22 homo sapien
43	151	6.5	574	2	Q8NGP7_HUMAN	Q8NGP7 homo sapien
44	150.5	6.5	1462	2	Q61ZR6_CABER	Q61ZR6 caenorhabdi
45	147.5	6.4	311	1	I20RB_HUMAN	Q6UX10 homo sapien

## ALIGNMENTS

RESULT 1  
INARI\_HUMAN STANDARD; PRT; 557 AA.  
AC P17181; Q8WTZ2;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-FEB-2005 (Rel. 46, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interferon-alpha/beta receptor alpha chain precursor (IPN-alpha-REC).  
GN Name=IFNAR1; Synonyms=IFNAR;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=90124632; PubMed=2153461;  
RA Uze G., Lutfalla G., Gresser I.;  
RT "Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";  
RL Cell 60:225-234(1990).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92129376; PubMed=1370833;  
RA Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;  
RT "The structure of the human interferon alpha/beta receptor gene.";  
RL J. Biol. Chem. 267:2802-2809(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-168; ILE-307 AND MET-359.  
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;  
RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";  
RL Submitted (JUN-04) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT VAL-168.  
TI Tissue=Brain;  
TX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.N., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.N., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RN PHOSPHORYLATION BY TYK2.  
 RX MEDLINE=95059042; PubMed=7526154;  
 RA Colamonic O., Yan H., Domanski P., Handa R., Smalley D.,  
 RA Mullersman J., Witte M., Krishnan K., Krolewski J.,  
 RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
 of the type I interferon receptor by p135tyk2 tyrosine kinase.";  
 RL Mol. Cell. Biol. 14:8133-8142(1994).  
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
 CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
 CC subunits themselves.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: IFN receptors are present in all tissues and  
 CC even on the surface of most IFN-resistant cells.  
 CC -1- PTM: Phosphorylated on tyrosine residues by TYK2 tyrosine kinase.  
 CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; J03171; AA52730.1; -; mRNA.  
 DR EMBL; X60459; CAA42992.1; -; Genomic DNA.  
 DR EMBL; AV654286; AAT49100.1; -; Genomic DNA.  
 DR EMBL; BC021825; AAH21825.1; -; mRNA.  
 DR EMBL; A32694; A32694.  
 DR Ensembl; ENSG00000142166; Homo sapiens.  
 DR HGNC; HGNC:5432; IFNAR1.  
 DR H-InvDB; HIX0016075; -.  
 DR MIM; 107450; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004905; F:interferon-alpha/beta receptor activity; TAS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.  
 DR GO; GO:0009615; P:response to virus; TAS.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR PROSITE; PS00853; FN3; FALSE\_NEG.  
 KW Glycoprotein; Phosphorylation; Polymorphism; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 557 Interferon-alpha/beta receptor alpha  
 FT chain.  
 FT TOPO\_DOM 28 436 Extracellular (Potential).  
 FT TRANSMEM 437 457 Potential.  
 FT TOPO\_DOM 458 557 Potential.  
 FT DOMAIN 134 224 Cytoplasmic (Potential).  
 FT DOMAIN 230 326 Fibronectin type-III 1.  
 FT DOMAIN 334 425 Fibronectin type-III 2.  
 FT MOD\_RES 466 466 Fibronectin type-III 3.  
 FT MOD\_RES 481 481 Phosphotyrosine (by TYK2) (Probable).  
 FT MOD\_RES 50 50 Phosphotyrosine (by TYK2) (Probable).  
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 81 81 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 314 314 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 416 416 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 433 433 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 79 87 By similarity.

FT DISULFID 199 220 By similarity.  
 FT VARIANT 168 168 L -> V.  
 FT VARIANT 307 307 /FTId=VAR\_002717.  
 FT VARIANT 359 359 V -> I.  
 FT VARIANT 359 359 /FTId=VAR\_020502.  
 FT CONFLICT 17 17 T -> M.  
 FT CONFLICT 17 17 /FTId=VAR\_020503.  
 FT SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75CBC CRC64;  
 SQ  
 Query Match 99.7%; Score 2307; DB 1; Length 557;  
 Best Local Similarity 99.8%; Pred. No. 3.1e-166;  
 Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MMVVLGATTLVLVAVGPVLSAAAGKNLKSPOKVEVDIIDNFTLRNRSDESVCNVT 60  
 DB 1 MMVVLGATTLVLVAVGPVLSAAAGKNLKSPOKVEVDIIDNFTLRNRSDESVCNVT 60  
 QY 61 FSPDYQKTGMNDWIKLSGCGNITSTKCNFSSLLKLVYEEIKLRIRAEKENTSSWYEVDSF 120  
 DB 61 FSPDYQKTGMNDWIKLSGCGNITSTKCNFSSLLKLVYEEIKLRIRAEKENTSSWYEVDSF 120  
 QY 121 TPFKRAQIGPPEVHLAEADKAIVIHISPTGKDSVMALDGLSFTYSLIIWKNSSGVEERI 180  
 DB 121 TPFKRAQIGPPEVHLAEADKAIVIHISPTGKDSVMALDGLSFTYSLIIWKNSSGVEERI 180  
 QY 181 ENIYSHKLYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
 DB 181 ENIYSHKLYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVQWLHAFILKRNPNHLYKWKQIPDCENVKTTQCVPQNVFQK 300  
 DB 241 NQNYVLKWDYTYANMTFQVQWLHAFILKRNPNHLYKWKQIPDCENVKTTQCVPQNVFQK 300  
 QY 301 GYLLRVQASDGNNTSFWESEIKFDTETIQAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 DB 301 GYLLRVQASDGNNTSFWESEIKFDTETIQAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 QY 361 VTQDPLIYEIIFWNTSNAERKIEKKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 361 VTQDPLIYEIIFWNTSNAERKIEKKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 DB 421 FSDAVCEKTKPGNTSK 436  
 RESULT 2  
 Q53H11 HUMAN  
 ID Q53H11\_HUMAN PRELIMINARY; PRT; 557 AA.  
 AC Q53H11\_HUMAN  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Interferon-alpha receptor 1 variant (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Maruyama K., Sugano S.;  
 RT "Oligo-capping: a simple method to replace the cap structure of  
 RT eucaryotic mRNAs with oligoribonucleotides.";  
 RL Gene 138:171-174(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;  
 RT "Construction and characterization of a full length-enriched and a 5'-  
 RT end-enriched cDNA library.";

```

RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA Tanaka A., Yokoyama S.;
RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK222770; BAD96490.1; -; mRNA.
KW Receptor.
FT NON TER
SQ SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75CBC CRC64;

Query Match 99.7%; Score 2307; DB 2; Length 557;
Best Local Similarity 99.8%; Pred. No. 3.1e-166;
Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRNRSDESNGVT 60
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRNRSDESNGVT 60
Qy 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSSLKLVYEEIKLIRAEKENTSSWYVDSF 120
Db 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSSLKLVYEEIKLIRAEKENTSSWYVDSF 120
Qy 121 TPFKAQIGPPEVHLEAEDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
Db 121 TPFKAQIGPPEVHLEAEDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
Qy 181 ENIYSRHKIYKLPETTYCLKVAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLPETTYCLKVAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240
Qy 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFQNVFQK 300
Db 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFQNVFQK 300
Qy 301 GIYLLRQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360
Db 301 GIYLLRQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360
Qy 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
Qy 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 3
Q53GW9 HUMAN PRELIMINARY; PRT; 557 AA.
AC Q53GW9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Interferon-alpha receptor 1 variant (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Maruyama K., Sugano S.;
RT "Oligo-capping: a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;

*Construction and characterization of a full length-enriched and a 5'-
end-enriched cDNA library.*;
Gene 200:149-156 (1997).
[3]
NUCLEOTIDE SEQUENCE.
TISSUE=Liver;
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
EMBL; AK222812; BAD96532.1; -; mRNA.
Receptor.
NON TER.
SEQUENCE 557 AA; 63598 MW; 2D9522BECC775486 CRC64;

Query Match 99.4%; Score 2300; DB 2; Length 557;
Best Local Similarity 99.3%; Pred. No. 1e-165;
Matches 433; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRNRSDESNGVT 60
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRNRSDESNGVT 60
Qy 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSSLKLVYEEIKLIRAEKENTSSWYVDSF 120
Db 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSSLKLVYEEIKLIRAEKENTSSWYVDSF 120
Qy 121 TPFKAQIGPPEVHLEAEDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
Db 121 TPFKAQIGPPEVHLEAEDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
Qy 181 ENIYSRHKIYKLPETTYCLKVAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLPETTYCLKVAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240
Qy 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFQNVFQK 300
Db 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFQNVFQK 300
Qy 301 GIYLLRQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360
Db 301 GIYLLRQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360
Qy 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFWENTSNARKEIEKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
Qy 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 4
Q6PKD7 HUMAN PRELIMINARY; PRT; 387 AA.
AC Q6PKD7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IFNARI protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarate P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smillius D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Strausberg R.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC002590; AAH02590.1; -: mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro: IPR000282; Cytok_receptor_2.
FT NON TER 387
SQ SEQUENCE 387 AA; 44388 MW; DEC1A8CC2F44499 CRC64;

Query Match 87.8%; Score 2030; DB 2; Length 387;
Best Local Similarity 99.5%; Pred. No. 1.9e-145;
Matches 381; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMVVLGATTLVLVAVGPVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGVT 60
DB 1 MMVVLGATTLVLVAVAPVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGVT 60

QY 61 FSPDYQKTGMNDIKLGGCQNTSTKCNFSLKLVYEEIKLIRAEKENTSSWYEDSF 120
DB 61 FSPDYQKTGMNDIKLGGCQNTSTKCNFSLKLVYEEIKLIRAEKENTSSWYEDSF 120

QY 121 TPRKQAIGPPEVHLEAEDKAIIVHISPGTKDSVMALDGLSTYSLLIWNSSGVEERI 180
DB 121 TPRKQAIGPPEVHLEAEDKAIIVHISPGTKDSVMALDGLSTYSLLIWNSSGVEERI 180

QY 181 ENIYSRHKIYKLPETTYCLVKVAALTSWKIGVSPVHCITKTVENELPPPNIEVSQ 240
DB 181 ENIYSRHKIYKLPETTYCLVKVAALTSWKIGVSPVHCITKTVENELPPPNIEVSQ 240

QY 241 NQNVYLKWDYTYANMTFQVQWLHAFKRNFGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
DB 241 NQNVYLKWDYTYANMTFQVQWLHAFKRNFGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300

QY 301 GIYLLRVQASDGNNTSPWSEIEIKFDTIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNT 360
DB 301 GIYLLRVQASDGNNTSPWSEIEIKFDTIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNT 360

QY 361 VIQDYPLIYELIIFWNTSNAERK 383
DB 361 VIQDYPLIYELIIFWNTSNAERK 383

RESULT 5
Q4R727 MACFA
ID Q4R727 MACFA PRELIMINARY; PRT; 477 AA.
AC Q4R727;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DE Testis cDNA, clone: OseA-16508, similar to human interferon (alpha,
DE beta and omega) receptor 1 (IFNARI), mRNA, RefSeq: NM_000629.2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
[1] NCBI_TaxID=9541;
RN NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Oeada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: AB169002; BAB01097.1; -: mRNA.
DR InterPro: IPR000282; Cytok_receptor_2.
KW Receptor; Transmembrane.
SQ SEQUENCE 477 AA; 54766 MW; 1D4110D471060BCF CRC64;

Query Match 73.5%; Score 1699.5; DB 2; Length 477;
Best Local Similarity 90.7%; Pred. No. 2.9e-120;
Matches 323; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 82 ITSTKCNFSSSLKLVYEEIKLIRAEKENTSSWYEDSFPPFKAQIGPPEVHLEAEDKA 141
DB 1 MSTKCNFSSSLKLVYDEIKLIRAEKENTSSWCEVDSFPFKAQIGPPEVHLEAEDKA 60

QY 142 IVIHIS-PGTQDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLPETTYCL 200
DB 61 IVIYISPPGTDSVMALDRSSFTYSLVIWNSSSVEERIENIYSRHKIYKLPETTYCL 120

QY 201 KYKAALLTSWKIGVSPVHCITKTVENELPPPNIEVSQNVQNYVLKWDYTYANMTFQVQ 260
DB 121 KYKAALLTSRKIGVSPVHCITKTVENELPPPNIEVIVQNYVLKWDYTYANMTFQVQ 180

QY 261 WLHAFKRNFGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWS 320
DB 181 WLHAFKRNFGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWS 240

QY 321 EIKFDTIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPTVIQDYPLIYELIIFWNTSNA 380
DB 241 EIKFDTIQAFLLPPVFNIRSLSDSLHSIGAPKSENKPVQDYPLIYELIIFWNTSKA 300

QY 381 ERKIETKTDVTVPNLKPLTVYCVKRAHMTDEKLNKSSVFSFSDAVCEKTPGNTSK 436
DB 301 ERKIETKTDVTVPNLKPLTVYCVKRAHMTDEKLNKSSVFSFSDVCEETKSGNTSK 356

RESULT 6
INARI_PIG
ID INARI_PIG STANDARD; PRT; 560 AA.
AC Q764M8;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
DE Name=IFNARI;
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=14681463; DOI=10.1093/nar/gkh037;
RA Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,
RA Okumura N., Hamasima N., Awata T.;
RT "PEDE (pig EST Data Explorer): construction of a database for ESTs
RT derived from porcine full-length cDNA libraries.";
RL Nucleic Acids Res. 32:D484-D488 (2004).
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type

```

I IFNs triggers tyrosine phosphorylation of a number of proteins including JAKs, TYK2, STAT proteins and IFN $\alpha$  and beta-subunits themselves (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Belongs to the type II cytokine receptor family.

-!- SIMILARITY: Contains 3 fibronectin type-III domains.

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EMBL; AB116561; BAD06315.1; -; mRNA.

InterPro; IPR000282; Cytok receptor\_2.

InterPro; IPR003961; FN III.

PROSITE; PS0853; FN3; FALSE NEG.

Glycoprotein; Receptor; Repeat; Signal; Transmembrane.

By similarity.

SIGNAL 1 24 Interferon-alpha/beta receptor alpha chain.

CHAIN 25 560

TOPO\_DOM 25 437 Extracellular (Potential).

TRANSMEM 438 458 Potential.

TOPO\_DOM 459 560 Cytoplasmic (Potential).

DOMAIN 133 224 Fibronectin type-III 1.

DOMAIN 230 326 Fibronectin type-III 2.

DOMAIN 334 426 Fibronectin type-III 3.

CARBOHYD 55 55 N-linked (GlcNAc. .) (Potential).

CARBOHYD 85 85 N-linked (GlcNAc. .) (Potential).

CARBOHYD 108 108 N-linked (GlcNAc. .) (Potential).

CARBOHYD 172 172 N-linked (GlcNAc. .) (Potential).

CARBOHYD 222 222 N-linked (GlcNAc. .) (Potential).

CARBOHYD 249 249 N-linked (GlcNAc. .) (Potential).

CARBOHYD 254 254 N-linked (GlcNAc. .) (Potential).

CARBOHYD 313 313 N-linked (GlcNAc. .) (Potential).

CARBOHYD 377 377 N-linked (GlcNAc. .) (Potential).

CARBOHYD 417 417 N-linked (GlcNAc. .) (Potential).

DISULFID 76 84 By similarity.

FT DISULFID 199 220 By similarity.

SQ SEQUENCE 560 AA; 63221 MW; DC193651033DFBDB CRC64;

Query Match 66.8%; Score 1546; DB 1; Length 560;  
Best Local Similarity 66.7%; Pred. No. 1.5e-108;  
Matches 293; Conservative 67; Mismatches 73; Indels 6; Gaps 5;

2 MVVLGATTLVLVAVGPNVLSAAGKVLKSPQKVEVDIIDDNFILRNWRSDESQVNTF 61  
1 MGLGLGATTLMLVAGAPVWL--PAGGADLRSPENVVSIIDDNFILRWKSSSVNTF 58  
62 SFYQKQGMNDWIKLSGCONITSTKCNFSSLLK-NVYEEIKLRIRAEKEN-TSSWYEYDS 119  
59 SADYQITGMNDWIKLPGQYVTSFTECNFSSIKLSKVYEKTKLRIRAEKGNSTSPWYVEP 118  
120 FTFPRKQIGPPEVHLEAEADKAIVHIS-PQTKDSVMWALDGLFTYSLIIWKNSGVVEE 178  
119 FIPQEAQIGPDPVHLEAEADKAIINTLSPPTKNSVMWAMSSSFVYSLVWKNSSSLE 178  
179 RIENYSHKYLKSPETTYCLKVKAALLTSWKGIVTSPVHCITVTENELPPENLEVS 238  
179 RKTQYARDKIHQSPETTYCLKVKAAGLRSPKGVSPVYCINTVVKHLPSPENLEIN 238  
239 VQONQYVLKWDYTYANMTFQVQLHAFILKRNPGNHLKWKQIPCCENVKTTQCVPFQNVF 298  
239 AENRVYVLKWNYYENVTFQVQLHAFILKPKEDHSDKWKQIPCCENVKTTCTHCVFQNVF 298  
299 QKGIYLLRVQASDGNNTSFWESEIKFDTETQAFLLPPVFNIRSLD-SFHYIYGAQKQSG 357  
299 TKGIFFIRVQASNGNSTSLWSEKRFNTEMQTILFPVPPVNNKPNINDASLRVIGAPKESE 358  
358 NTPVIQDPLIYEIIFWENTNABRKIIETKTDVTVNPKLTVYCVKARHTWDEKLNK 417  
359 DKSQNLQPLIYEIVFIRENTSDTERDVLKERTDFTFSNLKPLTVYCVKARALIENDRNWR 418

QY 418 SSVFSDAVCEKTKPGNTSK 436  
DB 419 SSVFSDTVCEKTKPGSTSQ 437

RESULT 7  
INARI\_BOVIN  
ID INARI\_BOVIN STANDARD; PRT; 560 AA.  
AC Q04790;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
GN Name=IFNARI; Synonyms=IFNAR;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Theria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=93076908; PubMed=1446745; DOI=10.1016/0014-5793(92)81204-Y;  
RA Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;  
RT "Specific antiviral activities of the human alpha interferons are determined at the level of receptor (IFNAR) structure."  
RL FEBS Lett. 313:255-259(1992).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93305725; PubMed=8318540; DOI=10.1016/0167-4781(93)90129-2;  
RA Lim J.-K., Langer J.A.;  
RT "Cloning and characterization of a bovine alpha interferon receptor."  
RL Biochim. Biophys. Acta 1173:314-319(1993).  
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type I IFNs triggers tyrosine phosphorylation of a number of proteins including JAKs, TYK2, STAT proteins and IFN $\alpha$  and beta-subunits themselves.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.

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EMBL; X68443; CAA48484.1; -; mRNA.  
EMBL; L08320; AAA02571.1; -; mRNA.  
PIR; S27387; S27387.  
InterPro; IPR000282; Cytok receptor\_2.  
InterPro; IPR003961; FN III.  
InterPro; IPR001187; Tissue factor.  
Pfam; PF01108; Tissue\_fac; 1.  
PROSITE; PS0853; FN3; 2.  
Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
By similarity.  
SIGNAL 1 24 Interferon-alpha/beta receptor alpha chain.  
CHAIN 25 560 Extracellular (Potential).

TOPO\_DOM 25 437 Potential.

TRANSMEM 438 458 Cytoplasmic (Potential).

TOPO\_DOM 459 560 Fibronectin type-III 1.

DOMAIN 133 224 Fibronectin type-III 2.

DOMAIN 230 326 Fibronectin type-III 3.

DOMAIN 334 426 N-linked (GlcNAc. .) (Potential).

CARBOHYD 47 47 N-linked (GlcNAc. .) (Potential).

CARBOHYD 55 55 N-linked (GlcNAc. .) (Potential).

CARBOHYD 85 85 N-linked (GlcNAc. .) (Potential).

CARBOHYD 109 109 N-linked (GlcNAc. .) (Potential).

CARBOHYD 172 172 N-linked (GlcNAc. .) (Potential).

CARBOHYD 254 254 N-linked (GlcNAc. .) (Potential).

CARBOHYD 313 313 N-linked (GlcNAc. .) (Potential).

CARBOHYD 377 377 N-linked (GlcNAc. .) (Potential).

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FT CARBOHYD 434 434 N-linked (GlcNAc... ) (Potential).
FT DISULFID 76 84 By similarity.
FT DISULFID 199 220 By similarity.
FT CONFLICT 422 422 F -> V (in Ref. 2).
SQ SEQUENCE 560 AA; 63918 MW; 66D76B72861E1D11 CRC64;

Query Match
Best Local Similarity 64.9%; Pred. No. 1.4e-105;
Matches 285; Conservative 65; Mismatches 83; Indels 6; Gaps 6;

QY 2 MVLGATTLVLVAVGPWVLSAAGGKVLKSPQKVEVDIIDDNFILWNRSDSVGNVTF 61
DB 1 MLALLGATTLMLVA-GRWVLPAAASGEANLK-PENVEIHIIIDNFFLKNSSSVGNVTF 58

QY 62 SFDYQKTMNDWIKLSGCONITSTKCNFSSKLK-NVYEEIKLRIRAEK-ENTSSWYEVD 119
DB SADYQILGTDNWKLPQCGOHIITSSKCNFSSVELKQVFEKIELIRAEENNTWTVEVEP 118

QY 120 FTFRKAQIGPPEVHLEAEDKAIVIHIS-PGTQDSVMWALDGLSFTYLLIWNSSGVVE 178
DB FVFPLEAQIGPPDVHLEAEDKAILISPPGTEDSIMWALDRSSFRYSVVIWNSSLEE 178

QY 179 RIENIYSRHKIYKLSPEITCYCLKVAALTSWKIGVSPVHCITKTVEVELPPENIEVS 238
DB RIETVPEDKIYKLSPEITCYCLKVAELKQSRVGCYSPVCIINTTERHKVSPENQIN 238

QY 239 VQONQYVLKWDYTYANMTFOVQWLHAFKRNPGNHLKWKQIPDCENVKTKQCFPQNVF 298
DB ADNQIYVLKWDYTYANMTFOQWLRAFPKIPGNHSDKWKQIPNCENVTSTHCVFPEVS 298

QY 299 QKGIYLRVQASDGNNTFSWSEIEKFTETIQAFLLPVPFNIRLS-DSPIYIYAPKQSG 357
DB SRGIYVRVRAASNGSGTSFWSEKEFTENKTIIFPPVIVSKVSTDLSLHVSVGASESE 358

QY 358 NTPVIQDPIYLIYELFWNTSNARKEIIEKTDVTVPNLKPLTYCVKARAHMTDEKLNK 417
DB NMSVNLQYLIYELFWNTSNARKEVLEKRTNFIIPDLKPLTYCVKARALIENDRRNK 418

QY 418 SSVFSDAACEKTPGNTSK 436
DB GSSFSDVCEKTPGNTSK 437

RESULT 8
ID INARI SHEEP STANDARD; PRT; 560 AA.
AC Q28589; Q95206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
DE (Interferon alpha/beta receptor-1).
GN Name=IFNAR1; Synonyms=IFNAR;
OS Ovis aries (Sheep).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=Endometrium;
RX MEDLINE=97135690; PubMed=8981227; DOI=10.1677/jme.0.0170207;
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in endometrium."
RL J. Mol. Endocrinol. 17:207-215(1996).
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TSSUE=Endometrium;
RX MEDLINE=98006426; PubMed=9348203; DOI=10.1210/en.138.11.4757;
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger
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RT ribonucleic acid for ovine receptors during the estrous cycle and pregnancy."
RL Endocrinology 138:4757-4767(1997).
CC 1- FUNCTION: Receptor for interferons alpha and beta. Binding to type I IFNs triggers tyrosine phosphorylation of a number of proteins including JAKs, TYK2, STAT proteins and IFN alpha- and beta- subunits themselves.
CC 1- SUBCELLULAR LOCATION: Type I membrane protein.
CC 1- TISSUE SPECIFICITY: Expressed in all tissues examined except conceptus at day 15 of pregnancy.
CC 1- SIMILARITY: Belongs to the type II cytokine receptor family.
CC 1- SIMILARITY: Contains 3 fibronectin type-III domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; X95939; CAA65183.1; -; mRNA.
DR EMBL; U65978; AAB84231.1; -; mRNA.
DR InterPro; IPR002822; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR PROSITE; PS00853; FN3; 3.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.
FT TOPO_DOM 25 437 Extracellular (Potential).
FT TRANSMEM 438 458 Potential.
FT TOPO_DOM 459 560 Cytoplasmic (Potential).
FT DOMAIN 125 224 Fibronectin type-III 1.
FT DOMAIN 230 326 Fibronectin type-III 2.
FT DOMAIN 330 426 Fibronectin type-III 3.
FT CARBOHYD 47 47 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 55 55 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 85 85 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 222 222 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 313 313 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 359 359 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 377 377 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 434 434 N-linked (GlcNAc... ) (Potential).
FT DISULFID 76 84 By similarity.
FT DISULFID 199 220 By similarity.
FT CONFLICT 352 352 S -> G (in Ref. 2).
FT CONFLICT 522 522 A -> D (in Ref. 2).
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

Query Match 65.0%; Score 1503; DB 1; Length 560;
Best Local Similarity 64.5%; Pred. No. 2.8e-105;
Matches 283; Conservative 68; Mismatches 82; Indels 6; Gaps 6;

QY 2 MVLGATTLVLVAVGPWVLSAAGGKVLKSPQKVEVDIIDDNFILWNRSDSVGNVTF 61
DB 1 MLGATTLMLVA-GRWVLPAAASGEANLK-ENVEIHIIIDNFFLKNSSSVGNVTF 58

QY 62 SFDYQKTMNDWIKLSGCONITSTKCNFSSKLK-NVYEEIKLRIRAEK-ENTSSWYEVD 119
DB SADYQILGTDNWKLPQCGOHIITSSKCNFSSVELKQVFEKIELIRAEENNTWTVEVEP 118

QY 120 FTFRKAQIGPPEVHLEAEDKAIVIHIS-PGTQDSVMWALDGLSFTYLLIWNSSGVVE 178
DB FVFPLEAQIGPPDVHLEAEDKAILISPPGTEDSIMWALDRSSFRYSVVIWNSSLEE 178

QY 179 RIENIYSRHKIYKLSPEITCYCLKVAALTSWKIGVSPVHCITKTVEVELPPENIEVS 238
DB RIETVPEDKIYKLSPEITCYCLKVAELKQSRVGCYSPVCIINTTERHKVSPENQIN 238

QY 239 VQONQYVLKWDYTYANMTFOVQWLHAFKRNPGNHLKWKQIPDCENVKTKQCFPQNVF 298
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Db 239 VDNQAYLVKWDYPYESTTFOAQLRAFLKIPGKHSNKWKQIPNCENVTTHCVFPRDIF 298
Qy 299 QKGIYLLRVQASDGNNTSFWSSEIKFDTETQAF 332
Db 299 SMGIYVVRVSRASNGTSGTFSWSEKEFTEVKLF 332
Qy 358 NTPVIQDPLIYELIFWNTSNAERKLEKTDVTPNLKPLTYVCVKAARHTWDEKLNK 417
Db 359 NMSYNQYPLVYEIFWNTSNAERKLEKTDVTPNLKPLTYVCVKAARHTWDEKLNK 418
Qy 418 SSVFSDAVCEKTKGNTSK 436
Db 419 GSSVSDVCEKTKGNTSK 437

RESULT 9
Q9GK86 SHEEP PRELIMINARY; PRT; 332 AA.
AC Q9GK86;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DB 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OS Type I interferon receptor 1e.
OC Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21267382; PubMed=11344274; DOI=10.1073/pnas.111139598;
RA Han C.S., Chen Y., Ezashi T., Roberts R.M.;
RT "Antiviral activities of the soluble extracellular domains of type I
interferon receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:6138-6143 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21267382; PubMed=11344274; DOI=10.1073/pnas.111139598;
RA Han C., Roberts M.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF296666; AAG42376.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN III.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00853; FN3; 2.
KW Receptor; Repeat; Transmembrane.
SQ SEQUENCE 332 AA; 38095 MW; 2CE7B93EC44B0E09 CRC64;

Query Match 49.9%; Score 1154.5; DB 2; Length 332;
Best Local Similarity 65.6%; Pred. No. 3.7e-79;
Matches 219; Conservative 49; Mismatches 61; Indels 5; Gaps 5;

Qy 2 MVVLGATTLVLVAGPWLVAAGGKLNKSPQKVEVDIIDNFIILRNWRSDESVGNVTF 61
Db 1 MSLILGATTLMLVA-GRWVLPASGEANLKS-ENVEITHIIDNFIILRNWRSDESVGNVTF 58
Qy 62 SFYQKTDGMDWIKLGGQNTITSKCNFSSKL-NVSEIKLRRAEK-ENTSWYEVDS 119
Db 59 SADIYQILGTDNRWKLPGCQHTSSKCNFSSVELKDVFEKIELRIRAEENNTSTWYVEP 118
Qy 120 FTPRKQIGPPEVHLRAEDKAIVTHIS-PTGKDSVMALDGLSTYLLWKNSSGVVEE 178
Db 119 FVPLKQIGPDPVHLEADKAILISLPPGTEDSIMALDRSFRYSVVIWKSSSLEE 178
Qy 179 RIENIYSRHKIYKLSPEITTYCLKVKAAALLTSWKIGVSPVHCITKTIVNELPPEPIEVS 238
Db 179 RTEITVPEDKIYKLSPEITTYCLKVKAEALQSRVGCYSPVICINTTERHKYSPENVQIN 238
Qy 239 VQNYVULKWDYTYANMTFQVOWHLAFILKRNPNHLYKWKQIPNCENVTTHCVFPRDIF 298
Db 239 VDNQAYLVKWDYPYESTTFOAQLRAFLKIPGKHSNKWKQIPNCENVTTHCVFPRDIF 298
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Db 239 VDNQAYLVKWDYPYESTTFOAQLRAFLKIPGKHSNKWKQIPNCENVTTHCVFPRDIF 298
Qy 299 QKGIYLLRVQASDGNNTSFWSSEIKFDTETQAF 332
Db 299 SMGIYVVRVSRASNGTSGTFSWSEKEFTEVKLF 332
Qy 358 NTPVIQDPLIYELIFWNTSNAERKLEKTDVTPNLKPLTYVCVKAARHTWDEKLNK 417
Db 359 NMSYNQYPLVYEIFWNTSNAERKLEKTDVTPNLKPLTYVCVKAARHTWDEKLNK 418
Qy 418 SSVFSDAVCEKTKGNTSK 436
Db 419 GSSVSDVCEKTKGNTSK 437

RESULT 10
ID INARI_MOUSE STANDARD; PRT; 590 AA.
AC P33896;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN Name=Ifnar1; Synonyms=Ifar, Ifnar;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92262522; PubMed=1533935;
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
in homospesific or heterospesific background."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
high-frequency rearrangements in the interferon-resistant L1210 cell
line."
RL Gene 148:343-346 (1994).
CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type
I IFNs triggers tyrosine phosphorylation of a number of proteins
including JAKs, TYK2, STAT proteins and IFN alpha- and beta-
subunits themselves.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; M89641; AAA37890.1; -; mRNA.
DR PIR; A45283; A45283.
DR Ensembl; ENSMUSG00000022967; Mus musculus.
DR MGI; MGI:107658; Ifnar1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN III.
DR PROSITE; PS00853; FN3; FALSE NEG.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 590 Interferon-alpha/beta receptor alpha
chain.
FT TOPO_DOM 27 429 Extracellular (Potential).
FT TRANSMEM 430 449 Potential.
FT TOPO_DOM 450 590 Cytoplasmic (Potential).
FT DOMAIN 134 224 Fibronectin type-III 1.
FT DOMAIN 230 327 Fibronectin type-III 2.
FT DOMAIN 335 418 Fibronectin type-III 3.
FT CARBOHYD 43 43 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 214 214 N-linked (GlcNAc. . .) (Potential).
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FT CARBOHYD 314 314 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 370 370 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 409 409 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 413 413 N-linked (GlcNAc. . .) (Potential).  
 FT DISULFID 78 86 By similarity.  
 FT DISULFID 199 220 By similarity.  
 SQ SEQUENCE 590 AA; 65777 MW; 7BC6DF370185D3A CRC64;  
 Query Match 46.2%; Score 1069; DB 1; Length 590;  
 Best Local Similarity 48.6%; Pred. No. 2.4e-72;  
 Matches 212; Conservative 77; Mismatches 137; Indels 10; Gaps 4;  
 QY 2 MVVLGATTLLVAVGPWVLSAAGGNKLSQPKVEVDIIDDNFILRNRSDES VGNVTF 61  
 Db 1 MLAVGAAALVLVAGAPWLPSPAAGGKLPENIDVYIIDDNYTLKWSHGSGSVTF 60  
 QY 62 SFQYQKTGMNDWIKLSQCNITSTKCNFSSKLNVYEEIKLIRAEKEN-TSSWYVDSP 120  
 Db 61 SAEYRTKDEAKWLKVPCEQHTTTTKCFSLDNTNVIKTQFRVRAEGNSTSSWNEVDPP 120  
 QY 121 TPFRKAQIGPPEVHLEAEKAIIVHISPGTKDSVWALDGLSFTYSLIWKNSGSGVEERI 180  
 Db 121 IPFYTAHMSPEVLEAEKAILVHISPPGQGNWALEKPSFYTIIRIWKSSSDKTTI 180  
 QY 181 ENIYSRHKIYKLPETTYCLVKAAALTSWKIGYSPVHCIKTTVENELPPPEIEVSQ 240  
 Db 181 NSTYVEKIPPELLPETTYCLEVRAIHPSLKSHSNSTVQICISTTVANKMPVGNLQVDAQ 240  
 QY 241 NQNVLYKWDY-TYANMTFOVQMLHAFKRNPGNHLKWKQIOPCENVKTTQCVFPQNVFQ 299  
 Db 241 GKSYVLKWDYIASADVLFRACQWLPVGYSKSGSGSHDKWKPIPTCANVQTHCVFSQDTVY 300  
 QY 300 KGIYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKSGNT 359  
 Db 301 TGTFHLLVQASDGNNTSFWSEEEKFIDSQKHLPPVITVTAMSDLLVTVNCQDSTCD- 359  
 QY 360 PVIQDYPLIYEIIFWENTSNAERKIEKKTDTVTVPNLKPLTYCVKARAHTMDKLNKSS 419  
 Db 360 -----GLNVEIIFWENTSNTKISMEKDGPEFTLKNLQPLTYCVQARV-LFRALLNKTS 412  
 QY 420 VFSDAVCEKTKPGNTS 435  
 Db 413 NFSEKLCETKTRPGSFS 428  
 RESULT 11  
 Q80UR8\_MOUSE PRELIMINARY; PRT; 590 AA.  
 AC Q80UR8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Interferon (Alpha and beta) receptor 1.  
 GN Names: Ifnari;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Hopkins R.F., Mariani K., Moore A.A., Rubin G.M., Hong L.,  
 RA Diatchenko L., Mardina K., Farmer A.A., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;  
 RA Strausberg R.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 DR EMBL; BC052217; AAHS2217.1; -; mRNA.  
 DR MGI; MGI:107659; Ifnari.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR SMART; SM00060; FN3; 3.  
 KW Receptor; Transmembrane.  
 SQ SEQUENCE 590 AA; 65713 MW; E8383FFA6BE3AF3C CRC64;  
 Query Match 45.9%; Score 1062; DB 2; Length 590;  
 Best Local Similarity 48.4%; Pred. No. 8.2e-72;  
 Matches 211; Conservative 77; Mismatches 138; Indels 10; Gaps 4;  
 QY 2 MVVLGATTLLVAVGPWVLSAAGGNKLSQPKVEVDIIDDNFILRNRSDES VGNVTF 61  
 Db 1 MLAVGAAALVLVAGAPWLPSPAAGGKLPENIDVYIIDDNYTLKWSHGSGSVTF 60  
 QY 62 SFQYQKTGMNDWIKLSQCNITSTKCNFSSKLNVYEEIKLIRAEKEN-TSSWYVDSP 120  
 Db 61 SAEYRTKDEAKWLKVPCEQHTTTTKCFSLDNTNVIKTQFRVRAEGNSTSSWNEVDPP 120  
 QY 121 TPFRKAQIGPPEVHLEAEKAIIVHISPGTKDSVWALDGLSFTYSLIWKNSGSGVEERI 180  
 Db 121 IPFYTAHMSPEVLEAEKAILVHISPPGQGNWALEKPSFYTIIRIWKSSSDKTTI 180  
 QY 181 ENIYSRHKIYKLPETTYCLVKAAALTSWKIGYSPVHCIKTTVENELPPPEIEVSQ 240  
 Db 181 NSTYVEKIPPELLPETTYCLEVRAIHPSLKSHSNSTVQICISTTVANKMPVGNLQVDAQ 240  
 QY 241 NQNVLYKWDY-TYANMTFOVQMLHAFKRNPGNHLKWKQIOPCENVKTTQCVFPQNVFQ 299  
 Db 241 GKSYVLKWDYIASADVLFRACQWLPVGYSKSGSGSDKWKPIPTCANVQTHCVFSQDTVY 300  
 QY 300 KGIYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKSGNT 359  
 Db 301 TGTFHLLVQASDGNNTSFWSEEEKFIDSQKHLPPVITVTAMSDLLVTVNCQDSTCD- 359  
 QY 360 PVIQDYPLIYEIIFWENTSNAERKIEKKTDTVTVPNLKPLTYCVKARAHTMDKLNKSS 419  
 Db 360 -----GLNVEIIFWENTSNTKISMEKDGPEFTLKNLQPLTYCVQARV-LFRALLNKTS 412  
 QY 420 VFSDAVCEKTKPGNTS 435  
 Db 413 NFSEKLCETKTRPGSFS 428  
 RESULT 12  
 Q80UJ3\_MOUSE PRELIMINARY; PRT; 590 AA.  
 ID Q80UJ3\_MOUSE  
 AC Q80UJ3;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Ifnari protein (Interferon (Alpha and beta) receptor 1).  
 GN Names: Ifnari;  
 OS Mus musculus (Mouse).





Qy 409 HTWDEKLNKSSVFSADVCEKTKPG 432  
 Db 422 --FSEAYNKSSDFSRRECIGTAGG 443

RESULT 14  
 Q5XPII\_CHICK PRELIMINARY; PRT; 569 AA.  
 AC Q5XPII;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Interferon receptor.  
 GN Name=IFNAR1;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Han C.-L., Wang M., Gao F., Wu Z.-G.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY744159; AAU93528.1; -; mRNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR00282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR SMART; SM00060; FN3; 3.  
 DR PROSITE; PSS0853; FN3; 4.  
 DR RECEPTOR.  
 KW Receptor.  
 SQ SEQUENCE 569 AA; 64093 MW; ABC89111A5476BFB CRC64;

Query Match 30.1%; Score 695.5; DB 2; Length 569;  
 Best Local Similarity 38.1%; Pred. No. 4.8e-44;  
 Matches 169; Conservative 76; Mismatches 172; Indels 27; Gaps 12;

Qy 7 GATTLVLVAVGPMVLSAAAGGNLKPQKVEVDIIDONFILRNWRSDSVGNVTESFDYQ 66  
 Db 9 GRLLAAVLLCVLVVSRCCAGTNLKSQDIQVAVDTNFTLMNNTGDT-NVTFSAQYQ 67

Qy 67 -----KTGMNDWIKLSGCONITSTKCNFSLKLNVEEIKLIRAE-KENTSSWYEVDSF 120  
 Db 68 CFDDLTQSEPEWKLSCQNVSHTECFSSAITAYYDTHIRIRAEEREAESPSSIFEM 127

Qy 121 TPRKQAIQGPPEVHLEAEDKAIVIHISPGTKDSV--MWALDGLSFTYSLIWNSSGVEE 178  
 Db 128 IPYEIAQIGPPETALQOSINGAIKINISPPPEANQVRKW-LISVFFKYNVVDNSSNV-E 185

Qy 179 RIENIYSRHKIKLSPETTYCLVKYKAAALLTSWKIGVYSPVHCIKTTVE-NELPPENIEV 237  
 Db 186 KVRSLPIDVINDLAPETTYCLVKQATVPLEDKGLFSPHICITRKVNDLLCPTNVRV 245

Qy 238 SVQNQNTVLKWDYTY-ANMTFQVQWLHAFKRNPGNHLKWKQIIPDCENVKTTQC----- 291  
 Db 246 FALNMKFYLLWDNHNHYEHVYTYQLTGYLKNLYDDYSKWKQVSGCENITSMKCNLSSV 305

Qy 292 VFPQNVFKGIYLLRVOASDGNNTSPWSEIKFDEIQAFLPPVFNIRSLSDSFHYIG 351  
 Db 306 IKPTS-----ASYFRVQAMNEYKNSCLSKDVEVDPPTNEIGPPDVKVDISDVLHIIKIT 361

Qy 352 APRQSGNTPVQDYPPLYEIIFFWENTSNAERKIIKKTD---VTVPNLKPITYVCVKARA 408  
 Db 362 PPGPGNKMISDLYDFYQIYLWNKSSDNBEVVKMKETQTATVSDLPASTLYCVKQVA 421

Qy 409 HTWDEKLNKSSVFSADVCEKTKPG 432  
 Db 422 --FSEAYNKSSDFSRRECIGTAGG 443

RESULT 15

Q9PVJ9\_CHICK PRELIMINARY; PRT; 442 AA.  
 AC Q9PVJ9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Interferon alpha/beta receptor 1 (Fragment).  
 GN Name=IFNAR1;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=99177346; PubMed=10077530;  
 RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;  
 RT "Comparative genomic analysis of the interferon/interleukin-10 receptor gene cluster."  
 RL Genome Res. 9:242-250(1999).  
 DR EMBL; AF082667; AAD13679.1; -; Genomic DNA.  
 DR Ensembl; ENSGALG00000015942; Gallus gallus.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR00282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PSS0853; FN3; 4.  
 DR RECEPTOR.  
 KW Receptor.  
 FT NON TER 442 442  
 SQ SEQUENCE 442 AA; 49877 MW; 839EBE92170609E0 CRC64;

Query Match 29.8%; Score 689.5; DB 2; Length 442;  
 Best Local Similarity 37.9%; Pred. No. 9.8e-44;  
 Matches 166; Conservative 77; Mismatches 168; Indels 27; Gaps 12;

Qy 7 GATTLVLVAVGPMVLSAAAGGNLKPQKVEVDIIDONFILRNWRSDSVGNVTFSFDYQ 66  
 Db 9 GRLLAAVLLCVLVVSRCCAGTNLKSQDIQVAVDTNFTLMNNTGDT-NVTFSAQYQ 67

Qy 67 -----KTGMNDWIKLSGCONITSTKCNFSLKLNVEEIKLIRAE-KENTSSWYEVDSF 120  
 Db 68 CFDDLTQSEPEWKLSCQNVSHTECFSSAITAYYDTHIRIRAEEREAESPSSIFEM 127

Qy 121 TPRKQAIQGPPEVHLEAEDKAIVIHISPGTKDSV--MWALDGLSFTYSLIWNSSGVEE 178  
 Db 128 IPYEIAQIGPPETALQOSINGAIKINISPPPEANQVRKW-LISVFFKYNVVDNSSNV-E 185

Qy 179 RIENIYSRHKIKLSPETTYCLVKYKAAALLTSWKIGVYSPVHCIKTTVE-NELPPENIEV 237  
 Db 186 KVRSLPIDVINDLAPETTYCLVKQATVPLEDKGLFSPHICITRKVNDLLCPTNVRV 245

Qy 238 SVQNQNTVLKWDYTY-ANMTFQVQWLHAFKRNPGNHLKWKQIIPDCENVKTTQC----- 291  
 Db 246 FALNMKFYLLWDNHNHYEHVYTYQLTGYLKNLYDDYSKWKQVSGCENITSMKCNLSSV 305

Qy 292 VFPQNVFKGIYLLRVOASDGNNTSPWSEIKFDEIQAFLPPVFNIRSLSDSFHYIG 351  
 Db 306 IKPTS-----ASYFRVQAMNEYKNSCLSKDVEVDPPTNEIGPPDVKVDISDVLHIIKIT 361

Qy 352 APRQSGNTPVQDYPPLYEIIFFWENTSNAERKIIKKTD---VTVPNLKPITYVCVKARA 408  
 Db 362 PPGPGNKMISDLYDFYQIYLWNKSSDNBEVVKMKETQTATVSDLPASTLYCVKQVA 421

Qy 409 HTWDEKLNKSSVFSADVCEKTKPG 426  
 Db 422 --FSEAYNKSSDFSRREC 437

Search completed: January 17, 2006, 07:18:42  
 Job time : 124.892 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:10:37 ; Search time 30.1828 Seconds  
(without alignments)  
1098.405 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKXKSPQKVEVDIIDNFI.....AHTMDEKLNKSVFSDAVCE 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	434	1	US-08-328-256-11
2	2141	100.0	436	1	US-08-307-588-2
3	2141	100.0	436	2	US-07-971-834-2
4	2141	100.0	436	2	US-09-240-675-2
5	2141	100.0	557	1	US-08-328-256-10
6	2141	100.0	557	1	US-08-471-454-2
7	2141	100.0	557	1	US-08-466-974-2
8	2141	100.0	557	1	US-08-471-453-2
9	2141	100.0	557	1	US-08-307-588-4
10	2141	100.0	557	2	US-07-971-834-4
11	2141	100.0	557	2	US-09-240-675-4
12	2141	100.0	557	2	US-09-949-016-5972
13	2138	99.9	575	2	US-09-949-016-8640
14	2124	99.2	631	2	US-09-056-461-22
15	2089	97.6	496	1	US-08-328-256-12
16	1093	51.1	226	2	US-08-871-572B-10
17	1048	48.9	224	2	US-08-871-572B-9
18	707	33.0	224	2	US-08-871-572B-13
19	672.5	31.4	227	2	US-08-871-572B-14
20	513.5	24.0	224	2	US-08-871-572B-11
21	490.5	22.9	202	4	PCT-US94-14277-3
22	452.5	21.1	219	2	US-08-871-572B-12
23	438.5	20.5	200	4	PCT-US94-14277-4
24	222	10.4	233	2	US-08-871-572B-8
25	220	10.3	273	2	US-09-949-016-11056
26	220	10.3	325	1	US-08-683-743-4
27	220	10.3	325	2	US-09-870-574-3

28	220	10.3	325	2	US-09-265-540E-6	Sequence 6, Appli
29	214	10.0	199	2	US-10-090-365-35	Sequence 35, Appli
30	214	10.0	199	2	US-09-728-911-35	Sequence 35, Appli
31	199	9.3	332	4	PCT-US94-14277-2	Sequence 2, Appli
32	192	9.0	223	4	PCT-US94-14277-6	Sequence 6, Appli
33	182	8.5	557	2	US-09-949-016-11502	Sequence 11502, A
34	180	8.4	553	1	US-08-943-087-2	Sequence 2, Appli
35	180	8.4	553	1	US-08-943-087-14	Sequence 14, Appli
36	180	8.4	553	1	US-08-943-087-16	Sequence 16, Appli
37	180	8.4	553	1	US-08-943-087-18	Sequence 18, Appli
38	180	8.4	553	1	US-08-943-087-20	Sequence 20, Appli
39	180	8.4	553	1	US-08-943-087-22	Sequence 22, Appli
40	180	8.4	553	1	US-08-943-087-24	Sequence 24, Appli
41	180	8.4	553	1	US-08-943-087-26	Sequence 26, Appli
42	180	8.4	553	1	US-08-943-087-28	Sequence 28, Appli
43	180	8.4	553	1	US-08-943-087-30	Sequence 30, Appli
44	180	8.4	553	1	US-08-943-087-32	Sequence 32, Appli
45	180	8.4	553	1	US-08-943-087-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1  
US-08-328-256-11  
; Sequence 11, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel  
; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-328-256-11

Query Match 100.0%; Score 2141; DB 1; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4.8e-213;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPOKVEVDIIDNFIILRWNRSDSVGNVTFSDYQKTMNDNWKLSGCONITSTK 60  
Db 27 GKNLKSPOKVEVDIIDNFIILRWNRSDSVGNVTFSDYQKTMNDNWKLSGCONITSTK 86  
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTFRKAQIGPPEVHLEAEDKAIIVIH 120  
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTFRKAQIGPPEVHLEAEDKAIIVIH 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVWLHAF 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVWLHAF 266  
Qy 241 KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 300  
Db 267 KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 326  
Qy 301 EIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

## RESULT 2

US-08-307-588-2  
; Sequence 2, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 436 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-307-588-2

Query Match 100.0%; Score 2141; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 4.8e-213;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPOKVEVDIIDNFIILRWNRSDSVGNVTFSDYQKTMNDNWKLSGCONITSTK 60  
Db 27 GKNLKSPOKVEVDIIDNFIILRWNRSDSVGNVTFSDYQKTMNDNWKLSGCONITSTK 86  
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTFRKAQIGPPEVHLEAEDKAIIVIH 120  
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTFRKAQIGPPEVHLEAEDKAIIVIH 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVWLHAF 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVWLHAF 266  
Qy 241 KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 300  
Db 267 KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEEIKFDT 326  
Qy 301 EIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

## RESULT 3

US-07-971-834-2  
; Sequence 2, Application US/07971834  
; Patent No. 6475983  
; GENERAL INFORMATION:  
; APPLICANT: EID, Pierre  
; APPLICANT: GRESSER, Ion  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: MEYER, Francois  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: TOVEY, Michael  
; APPLICANT: UZE, Gilles  
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH  
; TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/971,834  
; FILING DATE: 17-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR91/00318  
; FILING DATE: 17-APR-1991  
; ATTORNEY/AGENT INFORMATION:

```

; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-971-834-2

Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.8e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCQNIITSTK 60
Db 27 GKNLKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCQNIITSTK 86
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQIGPPEVHLEAEDKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQIGPPEVHLEAEDKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLIIWKNSSGVEERIENIYSRHKIYKLSPEYVHLEAEDKAIYIHI 180
Db 147 SPGTKDSVMWALDGLSFTYSLIIWKNSSGVEERIENIYSRHKIYKLSPEYVHLEAEDKAIYIHI 206
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 300
Db 267 KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 326
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTFVIQDYPLIYIIFWENTSNAERKIIIE 360
Db 327 EIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTFVIQDYPLIYIIFWENTSNAERKIIIE 386
Qy 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 4
US-09-240-675-2
; Sequence 2, Application US/09240675
; Patent No. 6787634
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; TITLE OF INVENTION: INTERFERON
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,675
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-240-675-2

Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.8e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCQNIITSTK 60
Db 27 GKNLKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCQNIITSTK 86
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQIGPPEVHLEAEDKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQIGPPEVHLEAEDKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLIIWKNSSGVEERIENIYSRHKIYKLSPEYVHLEAEDKAIYIHI 180
Db 147 SPGTKDSVMWALDGLSFTYSLIIWKNSSGVEERIENIYSRHKIYKLSPEYVHLEAEDKAIYIHI 206
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 300
Db 267 KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 326
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTFVIQDYPLIYIIFWENTSNAERKIIIE 360
Db 327 EIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTFVIQDYPLIYIIFWENTSNAERKIIIE 386
Qy 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 5
US-08-328-256-10
; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300

```

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; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL#13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-10

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Query Match      100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKMLSPQKVEVDIIDNFILRNRSDES VGNVTFSPDYQKTGMNWKLSGCONITSTK 60
Db 27 GKMLSPQKVEVDIIDNFILRNRSDES VGNVTFSPDYQKTGMNWKLSGCONITSTK 86
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKAIQIGPPEVHLEADKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKAIQIGPPEVHLEADKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNYVYLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNYVYLKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db 267 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326
Qy 301 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYIIFWNTSNAERKIIIE 360
Db 327 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYIIFWNTSNAERKIIIE 386
Qy 361 KKTDTVTPNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTPNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

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## RESULT 6

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US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges

```

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; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYENE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-454-2

Query Match      100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKMLSPQKVEVDIIDNFILRNRSDES VGNVTFSPDYQKTGMNWKLSGCONITSTK 60
Db 27 GKMLSPQKVEVDIIDNFILRNRSDES VGNVTFSPDYQKTGMNWKLSGCONITSTK 86
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKAIQIGPPEVHLEADKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKAIQIGPPEVHLEADKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNYVYLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNYVYLKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db 267 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326
Qy 301 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYIIFWNTSNAERKIIIE 360
Db 327 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYIIFWNTSNAERKIIIE 386
Qy 361 KKTDTVTPNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401

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Db 387 KKTDTVTVNKLPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 7

US-08-466-974-2

; Sequence 2, Application US/08466974

; Patent No. 5861258

; GENERAL INFORMATION:

; APPLICANT: MOGENSEN, Knud E.

; APPLICANT: UZE, Gilles

; APPLICANT: LUTFALLA, Georges

; APPLICANT: GRESSER, Ion

; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,974

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/900,642

; FILING DATE: 15-JUN-1992

; APPLICATION NUMBER: FR 89/13770

; FILING DATE: 20-OCT-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.

; REGISTRATION NUMBER: 32,205

; REFERENCE/DOCKET NUMBER: 960-7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-466-974-2

Query Match 100.0%; Score 2141; DB 1; Length 557;

Best Local Similarity 100.0%; Pred. No. 7.1e-213;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILNRNRSDESVGNVTFSFDYQKTGMNDWIKLSCQNITSTK 60

Db 27 GKNLSPQKVEVDIIDDNFILNRNRSDESVGNVTFSFDYQKTGMNDWIKLSCQNITSTK 86

Qy 61 CNFSSLKLVNVEIKLRRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIVIH 120

Db 87 CNFSSLKLVNVEIKLRRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIVIH 146

Qy 121 SPGTKDSVMWALDGLSFTSYLLIWNKSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 180

Db 147 SPGTKDSVMWALDGLSFTSYLLIWNKSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 206

Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANMTFQVWLHAPL 240

Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANMTFQVWLHAPL 266

Qy 241 KRNPENHLYKWKQIPDCENVKTTQCVPFQPNVQKGIYLLRVQASDGNNTSFWSSEIKPDT 300

Db 267 KRNPENHLYKWKQIPDCENVKTTQCVPFQPNVQKGIYLLRVQASDGNNTSFWSSEIKPDT 326

Qy 301 EIQAFLLPPVFNIRSLSDSFHVIYIGAPKQSGNTFVIQDYPILYIEIIIFWENTSNAERKIE 360

Db 327 EIQAFLLPPVFNIRSLSDSFHVIYIGAPKQSGNTFVIQDYPILYIEIIIFWENTSNAERKIE 386

Qy 361 KKTDTVTVNKLPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401

Db 387 KKTDTVTVNKLPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 8

US-08-471-453-2

; Sequence 2, Application US/08471453

; Patent No. 5886153

; GENERAL INFORMATION:

; APPLICANT: MOGENSEN, Knud E.

; APPLICANT: UZE, Gilles

; APPLICANT: LUTFALLA, Georges

; APPLICANT: GRESSER, Ion

; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,453

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/900,642

; FILING DATE: 15-JUN-1992

; APPLICATION NUMBER: FR 89/13770

; FILING DATE: 20-OCT-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.

; REGISTRATION NUMBER: 32,205

; REFERENCE/DOCKET NUMBER: 960-7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-471-453-2

Query Match 100.0%; Score 2141; DB 1; Length 557;

Best Local Similarity 100.0%; Pred. No. 7.1e-213;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILNRNRSDESVGNVTFSFDYQKTGMNDWIKLSCQNITSTK 60

Db 27 GKNLSPQKVEVDIIDDNFILNRNRSDESVGNVTFSFDYQKTGMNDWIKLSCQNITSTK 86

Qy 61 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 146  
Qy 121 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 180  
Db 147 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 206  
Qy 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQYVVKWDVYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQYVVKWDVYANMTFQVQWLHAF 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
Qy 301 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTVPIQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTVPIQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 9  
US-08-307-588-4  
; Sequence 4, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-307-588-4

Query Match 100.0%; Score 2141; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 7.1e-213; Indels 0; Gaps 0;  
Matches 401; Conservative 0; Mismatches 0;  
Qy 1 GKNLKSPQKVEVDIIDNFIILRNWRSDES VGNVTFSPFDYQKTGMNDWIKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDIIDNFIILRNWRSDES VGNVTFSPFDYQKTGMNDWIKLSGCONITSTK 86  
Qy 61 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 146  
Qy 121 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 180  
Db 147 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 206  
Qy 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQYVVKWDVYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQYVVKWDVYANMTFQVQWLHAF 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
Qy 301 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTVPIQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTVPIQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 10  
US-07-971-834-4  
; Sequence 4, Application US/07971834  
; Patent No. 6475983  
; GENERAL INFORMATION:  
; APPLICANT: EID, Pierre  
; APPLICANT: GRESSER, Ion  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: MEYER, Francois  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: TOVEY, Michael  
; APPLICANT: UZE, Gilles  
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH  
; TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/971,834  
; FILING DATE: 17-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR91/00318  
; FILING DATE: 17-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: EID=1  
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-971-834-4

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNWKLSGCONITSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNWKLSGCONITSTK 86

Qy 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 120
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 146

Qy 121 SPGKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180
Db 147 SPGKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206

Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNHLYKWKOIPDCENVKTCQVFPQNVFGIYLLRVOASDGNNTSFSWSEIKEDT 300
Db 267 KRNPNHLYKWKOIPDCENVKTCQVFPQNVFGIYLLRVOASDGNNTSFSWSEIKEDT 326

Qy 301 EIQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYELIIFWENTSNAERKIL 360
Db 327 EIQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYELIIFWENTSNAERKIL 386

Qy 361 KKTDTVTNPKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTNPKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 11
US-09-240-675-4
; Sequence 4, Application US/09240675
; Patent No. 6787634
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,675
; FILING DATE:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 207012

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; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-240-675-4

Query Match 100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNWKLSGCONITSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNWKLSGCONITSTK 86

Qy 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 120
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 146

Qy 121 SPGKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180
Db 147 SPGKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206

Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNHLYKWKOIPDCENVKTCQVFPQNVFGIYLLRVOASDGNNTSFSWSEIKEDT 300
Db 267 KRNPNHLYKWKOIPDCENVKTCQVFPQNVFGIYLLRVOASDGNNTSFSWSEIKEDT 326

Qy 301 EIQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYELIIFWENTSNAERKIL 360
Db 327 EIQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQDYPLIYELIIFWENTSNAERKIL 386

Qy 361 KKTDTVTNPKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTNPKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 12
US-09-949-016-5972
; Sequence 5972, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5972
; LENGTH: 557
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-5972

Query Match
  100.0%; Score 2141; DB 2; Length 557;
Best Local Similarity 100.0%; Pred. No. 7.1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDNFIILNRSDSGVNTFFSDYQKTMNDWIKLGGCQNTSTK 60
Db 27 GKNLKSPQKVEVDIIDNFIILNRSDSGVNTFFSDYQKTMNDWIKLGGCQNTSTK 86
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLAEADKAIYIHI 120
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLAEADKAIYIHI 146
Qy 121 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180
Db 147 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326
Qy 301 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPYLIYIIFWENTSNAERKIE 360
Db 327 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPYLIYIIFWENTSNAERKIE 386
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 13
US-09-949-016-8640
; Sequence 8640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8640
; LENGTH: 575
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-8640

Query Match
  99.9%; Score 2138; DB 2; Length 575;
Best Local Similarity 99.8%; Pred. No. 1.5e-212;
Matches 400; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDNFIILNRSDSGVNTFFSDYQKTMNDWIKLGGCQNTSTK 60
Db 45 GKNLKSPQKVEVDIIDNFIILNRSDSGVNTFFSDYQKTMNDWIKLGGCQNTSTK 104
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Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLAEADKAIYIHI 120
Db 105 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLAEADKAIYIHI 164
Qy 121 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180
Db 165 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 224
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240
Db 225 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 284
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300
Db 285 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 344
Qy 301 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPYLIYIIFWENTSNAERKIE 360
Db 345 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPYLIYIIFWENTSNAERKIE 404
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
Db 405 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 445

RESULT 14
US-09-056-461-22
; Sequence 22, Application US/09056461
; Patent No. 6713609
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anon
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Love, Richard B.
; APPLICANT: Lu, Ji
; APPLICANT: Stewart, Timothy A.
; TITLE OF INVENTION: Type I Interferon Receptor Antibodies
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,461
; FILING DATE: 07-Apr-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/058212
; FILING DATE: 16
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1039P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-461-22

Query Match
  99.2%; Score 2124; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 5e-211;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 LKSPQKVEVDIIDDNFILRNRSDESVCNVTFSFDYQKTGMNDWIKLSGCONITSTKCNF 63  
DB 1 LKSPQKVEVDIIDDNFILRNRSDESVCNVTFSFDYQKTGMNDWIKLSGCONITSTKCNF 60  
QY 64 SSLKLNVEEIKLIRAEKENTSSWYEVDSFTPRKQAGIPPEVHLEAEDKAIIVHISPG 123  
DB 61 SSLKLNVEEIKLIRAEKENTSSWYEVDSFTPRKQAGIPPEVHLEAEDKAIIVHISPG 120  
QY 124 TKDSVMALDGLSTYSLLIWNSSGVEERENIYSRHKIYKLSPEPTYCYLKVKAAALTS 183  
DB 121 TKDSVMALDGLSTYSLLIWNSSGVEERENIYSRHKIYKLSPEPTYCYLKVKAAALTS 180  
QY 184 WKIGVSPVHCICKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAFKRN 243  
DB 181 WKIGVSPVHCICKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAFKRN 240  
QY 244 PGNHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKFDTEIQ 303  
DB 241 PGNHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKFDTEIQ 300  
QY 304 AFLPPVFNIRSLSDSFHYIYGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERKIIIEKT 363  
DB 301 AFLPPVFNIRSLSDSFHYIYGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERKIIIEKT 360  
QY 364 DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 361 DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 398

## RESULT 15

US-08-328-256-12  
; Sequence 12, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel  
; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; NAME: BROWDY, Roger L.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 496 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

! MOLECULE TYPE: protein  
US-08-328-256-12

Query Match 97.6%; Score 2089; DB 1; Length 496;  
Best Local Similarity 98.0%; Pred. No. 1.5e-207;  
Matches 393; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
QY 1 GKNLKSPQKVEVDIIDDNFILRNRSDESVCNVTFSFDYQKTGMNDWIKLSGCONITSTK 60  
DB 27 GKNLKSPQKVEVDIIDDNFILRNRSDESVCNVTFSFDYQKTGMNDWIKLSGCONITSTK 86  
QY 61 CNFSSLLKNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAGIPPEVHLEAEDKAIIVHI 120  
DB 87 CNFSSLLKNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAGIPPEVHLEAEDKAIIVHI 146  
QY 121 SPGTKDSVMALDGLSTYSLLIWNSSGVEERENIYSRHKIYKLSPEPTYCYLKVKAAAL 180  
DB 147 SPGTKDSVMALDGLSTYSLLIWNSSGVEERENIYSRHKIYKLSPEPTYCYLKVKAAAL 206  
QY 181 LTSWKIGVSPVHCICKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 240  
DB 207 LTSWKIGVSPVHCICKTTVENELPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 266  
QY 241 KRNPNGHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKE 300  
DB 267 KRNPNGHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKE 326  
QY 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERK 360  
DB 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERK 386  
QY 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTPNLKPLTVYCVKARAHTMDE-----SDAVCE 419

Search completed: January 17, 2006, 07:20:57  
Job time : 31.1828 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 06:24:56 ; Search time 135 Seconds  
(without alignments)  
1419.031 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVLGATTLVLAQWV.....KSSVFSDAVCEKPGNTSK 436

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2313	100.0	436	2 AAR14487	Aar14487 Soluble i
2	2313	100.0	436	2 AAR28495	Aar28495 Sequence
3	2313	100.0	436	6 ABU05090	Abu05090 Human exp
4	2313	100.0	436	6 ABU05092	Abu05092 Human exp
5	2313	100.0	436	6 ABU05098	Abu05098 Human exp
6	2313	100.0	557	2 AAR14488	Aar14488 Complete
7	2313	100.0	557	2 AAR11958	Aar11958 Human alp
8	2313	100.0	557	2 AAR28496	Aar28496 Sequence
9	2313	100.0	557	2 AAR42635	Aar42635 Human int
10	2313	100.0	557	6 ABU05091	Abu05091 Human exp
11	2313	100.0	557	6 ABU05094	Abu05094 Human exp
12	2313	100.0	557	6 ABU05107	Abu05107 Human exp
13	2313	100.0	557	6 ABU05099	Abu05099 Human exp
14	2313	100.0	557	6 ABU05106	Abu05106 Human exp
15	2313	100.0	557	6 ABU05097	Abu05097 Human exp
16	2313	100.0	557	6 ABU05093	Abu05093 Human exp
17	2313	100.0	557	6 ABU05100	Abu05100 Human exp
18	2313	100.0	575	8 ADR666319	Adr666319 Human pro
19	2313	100.0	575	8 ADR66661	Adr66661 Human pro
20	2309	99.8	557	6 AAR75356	Aar75356 Human IFN
21	2309	99.8	557	6 ABU05102	Abu05102 Human exp
22	2308	99.8	557	2 AAW21804	Aaw21804 Transmemb
23	2308	99.8	557	6 ABU05103	Abu05103 Human exp
24	2307	99.7	557	6 ABU05095	Abu05095 Human exp

25	2304	99.6	436	2 AAR71723	Aar71723 IFN recep
26	2304	98.6	436	6 ABU05101	Abu05101 Human exp
27	2302	99.5	575	3 AAB57094	Aab57094 Human pro
28	2302	99.5	575	6 ABU05096	Abu05096 Human exp
29	2287	98.9	575	4 ABG17294	Abg17294 Novel hum
30	2279	98.5	441	9 ADV25067	Adv25067 INR1_T11
31	2260	97.7	434	2 AAW21805	Aaw21805 Spliced-d
32	2260	97.7	434	6 ABU05104	Abu05104 Human exp
33	2208	95.5	496	2 AAW21806	Aaw21806 Spliced-d
34	2208	95.5	496	6 ABU05105	Abu05105 Human exp
35	2158	93.3	631	8 ADK23579	Adk23579 Human IFN
36	1725.5	74.6	458	8 ADH22370	Adh22370 Human rec
37	916	39.6	187	8 ADH22369	Adh22369 Human rec
38	236.5	10.2	273	6 ABR38950	AbR38950 Human AK1
39	234.5	10.1	273	6 ABR38949	AbR38949 Human AK1
40	233.5	10.1	220	5 AAU76911	Aau76911 Human cyt
41	233.5	10.1	220	8 ADS31753	Ads31753 Human CRF
42	233.5	10.1	220	8 ADS92755	Ads92755 Human CRF
43	233.5	10.1	273	6 ABR38944	AbR38944 Human AK1
44	233.5	10.1	476	5 AAU76912	Aau76912 Human CRF
45	233.5	10.1	476	6 AAe30845	Aae30845 Human CRF

## ALIGNMENTS

RESULT 1  
AAR14487  
ID AAR14487 standard; protein; 436 AA.  
XX AC AAR14487;  
XX DT 16-JAN-1992 (first entry)  
XX DE Soluble interferon-alpha/beta receptor.  
XX KW IFN; autoimmune disease; graft rejection; histocompatibility.  
XX OS Homo sapiens.  
XX PN FR2657881-A.  
XX PD 09-AUG-1991.  
XX PF 05-FEB-1990; 90FR-00001298.  
XX PR 05-FEB-1990; 90FR-00001298.  
XX PA (EUBI-) LAB EURO BIOTECHNO.  
XX PI Bid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG; Uze G;  
XX DR WPI; 1991-319778/44.  
XX PS N-PSDB; AAQ14239.  
XX PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
XX used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
XX anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX PS Claim 2; Page 45; 52pp; French.  
XX CC The transmembrane and cytoplasmic domains of the native IFN receptor have  
XX been deleted to obtain a soluble, circulating form of the receptor.  
XX CC Potentially immunogenic epitopes have thus been eliminated. Derivatives  
XX obtained by substitution or deletion of this sequence are also claimed as  
XX are hybrid molecules comprising the soluble receptor (or deriv.) and an  
XX immunoglobulin such as IgG1. See also AAQ14240  
SQ Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 2; Length 436;  
Best Local Similarity 100.0%; Pred. No. 7e-200;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNTT 60  
DB 1 MMVLLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNTT 60

QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
DB 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300

QY 301 GYLLRVQASDGNNTSFWESEIKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
DB 301 GYLLRVQASDGNNTSFWESEIKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

QY 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 2  
AAR28495  
ID AAR28495 standard; protein; 436 AA.

XX AC AAR28495;  
XX DT 25-MAR-2003 (revised)  
XX DT 31-MAR-1993 (first entry)  
XX DE Sequence of a soluble form of the interferon (IFN) receptor with a high  
XX DE affinity for IFN-alpha and -beta.  
XX KW Interferon receptor; alpha-interferon; beta-interferon.  
XX OS Synthetic.  
XX PN WO9218626-A1.  
XX PD 29-OCT-1992.  
XX PF 17-APR-1991; 91WO-FR000318.  
XX PR 17-APR-1991; 91WO-FR000318.  
XX PA (EUBI-) LAB EURO BIOTECHNOLOGIE.  
XX PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
XX PI Uze G;  
XX XX  
XX DR WPI; 1992-382110/46.  
XX DR N-PSDB; AAQ30532.  
XX PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
XX PT useful as immunosuppressants, for treating autoimmune diseases and  
XX PT transplant rejection.  
XX PS Claim 2; Fig 1; 58pp; English.  
XX XX

CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
CC primers and cloned cDNA as template. For example, bacteriophage lambda  
CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.  
CC AAR28496 represents the complete receptor. AAR28495 lacks the  
CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
CC diseases and graft rejection. They lack the toxic side-effects of known  
CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX SQ Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 2; Length 436;  
Best Local Similarity 100.0%; Pred. No. 7e-200;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNTT 60  
DB 1 MMVLLGATTLVAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNTT 60

QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
DB 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300

QY 301 GYLLRVQASDGNNTSFWESEIKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
DB 301 GYLLRVQASDGNNTSFWESEIKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

QY 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 3  
ABU05090  
ID ABU05090 standard; protein; 436 AA.

XX AC ABU05090;  
XX DT 29-JAN-2003 (first entry)  
XX XX  
XX DE Human expressed protein tag (EPT) #1756.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;  
XX KW receptor; transcription factor; cancer; MHC;  
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX XX

PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
XX Chiciz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1756; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 436 AA;  
SQ

Query Match 100.0%; Score 2313; DB 6; Length 436;  
Best Local Similarity 100.0%; Pred. No. 7e-200;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPVWLSAAAGGKLNKSPQKVEVDIIDDNFILRNRSDESNGVT 60  
DB 1 MMVLLGATTLVAVGPVWLSAAAGGKLNKSPQKVEVDIIDDNFILRNRSDESNGVT 60

QY 61 FSPDYQKGMWNWIKLGGCONITSTKCNFSSKLNVYRKIRAEKENTSSWYEVDSF 120  
DB 61 FSPDYQKGMWNWIKLGGCONITSTKCNFSSKLNVYRKIRAEKENTSSWYEVDSF 120

QY 121 TPFRAQIGPEVHLEAEKAIIVIHISPTGKDSVMWALDGLSPTYLLWKSSGVEERI 180  
DB 121 TPFRAQIGPEVHLEAEKAIIVIHISPTGKDSVMWALDGLSPTYLLWKSSGVEERI 180

QY 181 ENIYSRHKYKLSPTYCYLKVKAALLTSWKIGVSPVHCITVTENELPPENIEVSQ 240  
DB 181 ENIYSRHKYKLSPTYCYLKVKAALLTSWKIGVSPVHCITVTENELPPENIEVSQ 240

QY 241 NQNYLKWDTYANMTFQWHLAFKRNPGNHLKWKQIPDCENKTTQCVPPQNVQK 300  
DB 241 NQNYLKWDTYANMTFQWHLAFKRNPGNHLKWKQIPDCENKTTQCVPPQNVQK 300

QY 301 GYLLRVQASDGNNTSFWSSEIEKFTDEIOAFLLPVFNIRSLSDSPHIVIGAPKQSGNTP 360  
DB 301 GYLLRVQASDGNNTSFWSSEIEKFTDEIOAFLLPVFNIRSLSDSPHIVIGAPKQSGNTP 360

QY 361 VIQDYLPIYEIIFWENTSNAERKIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYLPIYEIIFWENTSNAERKIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 4  
ABU05092  
ID ABU05092 standard; protein; 436 AA.  
XX  
AC ABU05092;  
XX  
XX 29-JAN-2003 (first entry)  
XX  
XX Human expressed protein tag (EPT) #1758.  
XX  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
XX Homo sapiens.  
OS  
XX WO200278524-A2.  
PN  
XX 10-OCT-2002.  
PD  
XX 28-MAR-2002; 2002WO-US009671.  
PP  
XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chiciz RM, Tomlinson AJ, Urban RG;  
PI  
XX WPI; 2003-040607/03.  
DR

New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1758; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 436 AA;  
SQ

Query Match 100.0%; Score 2313; DB 6; Length 436;  
Best Local Similarity 100.0%; Pred. No. 7e-200;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGPWVLSAAGGKNLKSPOKVEVDIIDDNFILRNRSDESQVNT 60  
 Db 1 MMVLLGATTLVLVAVGPWVLSAAGGKNLKSPOKVEVDIIDDNFILRNRSDESQVNT 60  
 QY 61 FSPDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120  
 Db 61 FSPDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
 Db 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
 Db 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
 Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
 QY 301 GIYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
 Db 301 GIYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
 QY 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
 Db 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 5

ABU05098  
 ID ABU05098 standard; protein; 436 AA.  
 XX AC ABU05098;  
 XX DT 29-JAN-2003 (first entry)  
 XX DE Human expressed protein tag (EPT) #1764.  
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW processase; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX OS Homo sapiens.  
 XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX PF 28-MAR-2002; 2002WO-US009671.  
 XX PR 28-MAR-2001; 2001US-0279495P.  
 XX PR 21-MAY-2001; 2001US-0292544P.  
 XX PR 08-AUG-2001; 2001US-0310801P.  
 XX PR 01-OCT-2001; 2001US-0326370P.  
 XX PR 04-DEC-2001; 2001US-0336780P.  
 XX PR 20-FEB-2002; 2002US-035985P.  
 XX PA (ZYCO-) ZYCOS INC.  
 XX PI Chicx RM, Tomlinson AJ, Urban RG;  
 XX WPI; 2003-040607/03.  
 XX DE New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX Example 2; SEQ ID NO 1764; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 6; Length 436;

Best Local Similarity 100.0%; Pred. No. 7e-200;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGPWVLSAAGGKNLKSPOKVEVDIIDDNFILRNRSDESQVNT 60  
 Db 1 MMVLLGATTLVLVAVGPWVLSAAGGKNLKSPOKVEVDIIDDNFILRNRSDESQVNT 60

QY 61 FSPDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120

Db 61 FSPDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120

QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180

Db 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240

Db 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300

Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300

QY 301 GIYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

Db 301 GIYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

QY 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Db 361 VIQDYPLIYEIIFWENTSNARKEIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436

Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 6

AAR14488  
 ID AAR14488 standard; protein; 557 AA.

XX AC AAR14488;

XX DT 16-JAN-1992 (first entry)

XX DE Complete interferon-alpha/beta receptor.

XX KW IFN; autoimmune disease; graft rejection; histocompatibility.



XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Domain 437..457  
 FT Domain /label= transmembrane  
 FT Domain 458..557  
 FT Domain /label= cytoplasmic  
 XX FR2657881-A.  
 XX PD 09-AUG-1991.  
 XX PF 05-FEB-1990; 90FR-00001298.  
 XX PR 05-FEB-1990; 90FR-00001298.  
 XX PA (EUBI-) LAB EURO BIOTECHNO.  
 XX PI Bid P, Gresser I, Lutfalla G, Meyer P, Mogensen KE, Tovey MG;  
 PI Uze G;  
 XX WPI; 1991-319778/44.  
 DR N-PSDB; AAQ14240.  
 XX New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
 PT used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
 PT anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
 XX Disclosure; Page 47; 52pp; French.  
 XX The invention covers derivatives of the interferon-alpha and/or beta  
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains  
 CC of the native receptor or by substitution. Potentially immunogenic  
 CC epitopes are eliminated and the deriv. can be secreted from transformed  
 CC cells. Soluble deriv.s block the activity of IFN alpha/beta and can be  
 CC used to treat autoimmune diseases or to inhibit graft rejection. See also  
 CC AAQ14239  
 XX  
 SQ Sequence 557 AA;  
 Query Match 100.0%; Score 2313; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
 QY 61 FSFDYQKTGMNDWIKLGGQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 DB 61 FSFDYQKTGMNDWIKLGGQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENKTKTQCVPPQNVFOK 300  
 DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENKTKTQCVPPQNVFOK 300  
 QY 301 GYLRLVQASDGNNTSFWSSEIKFDEIOAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 DB 301 GYLRLVQASDGNNTSFWSSEIKFDEIOAFLLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 QY 361 VIQDPLIYIIFWNTSNAERKIEKKTDTVPVNLKPLTYCVKARAHTMDKLNKSSV 420  
 DB 361 VIQDPLIYIIFWNTSNAERKIEKKTDTVPVNLKPLTYCVKARAHTMDKLNKSSV 420

QY 421 FSDAVCEKTKPNTSK 436  
 DB 421 FSDAVCEKTKPNTSK 436  
 RESULT 7  
 ID AAR11958  
 XX AAR11958 standard; protein; 557 AA.  
 XX AC AAR11958;  
 XX DT 18-JUL-1991 (first entry)  
 XX DE Human alpha-interferon receptor protein.  
 XX KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;  
 XX KW drug targeting.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..27  
 FT /label= signal peptide  
 XX WO9105862-A.  
 XX PD 02-MAY-1991.  
 XX PF 20-OCT-1989; 89FR-00013770.  
 XX PR 20-OCT-1989; 89FR-00013770.  
 XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PI Mogensen K, Lutfalla G, Gresser I;  
 XX WPI; 1991-148740/20.  
 DR N-PSDB; AAQ11701.  
 XX New human alpha-interferon receptor protein - useful for testing  
 FT interferon agonists and in treatment or diagnosis.  
 XX Disclosure; Fig 4; 30pp; French.  
 XX This recombinant human alpha interferon (IFN) receptor protein is useful  
 CC for the testing of IFN agonists and for treatment and diag- nosis of  
 CC viral diseases and tumours. Antibodies raised against this protein can be  
 CC used for blocking the receptor when required, eg where overexpression of  
 CC alpha-IFN is harmful. The Abs are also useful for eg drug targeting.  
 CC Variants of the protein, having residue 164 (Thr) replaced by Arg and an  
 CC Asp inserted between residues 479 and 480, are also useful  
 XX  
 SQ Sequence 557 AA;  
 Query Match 100.0%; Score 2313; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
 QY 61 FSFDYQKTGMNDWIKLGGQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 DB 61 FSFDYQKTGMNDWIKLGGQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240

QY 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 Db 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 QY 361 VTQDYPLIYEIIFWNTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARHTMDEKLNKSSV 420  
 Db 361 VTQDYPLIYEIIFWNTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARHTMDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 8

AAR28496  
 ID AAR28496 standard; protein; 557 AA.

XX AAR28496;  
 AC AAR28496;

XX 25-MAR-2003 (revised)  
 DT 31-MAR-1993 (first entry)

XX Sequence of a soluble form of the interferon (IFN) receptor with a high

DE affinity for IFN-alpha and -beta.  
 DE Interferon receptor; alpha-interferon; beta-interferon.

XX Synthetic.

XX WO9218626-A1.

XX 29-OCT-1992.

XX 17-APR-1991; 91WO-FR000318.

XX 17-APR-1991; 91WO-FR000318.

XX (EUBI-) LAB EURO BIOTECHNOLOGIE.

XX Bid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;

PI Uze G;

XX WPI; 1992-382110/46.

DR N-PSDB; AAQ30533.

XX Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
 PT useful as immunosuppressants, for treating auto-immune diseases and  
 PT transplant rejection.

XX Claim 3; Fig 2; 58pp; English.

XX DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
 CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
 CC primers and cloned cDNA as template. For example, bacteriophage lambda  
 CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
 CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.  
 CC AAR28496 represents the complete receptor. AAR28495 lacks the  
 CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
 CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
 CC diseases and graft rejection. They lack the toxic side-effects of known  
 CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
 CC PN field.)

XX Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLLVAVGPNVLSSAAGGKNLKSPOKVEVDIIDDNFIILNRSDSVGNVT 60  
 Db 1 MMVLLGATTLLVAVGPNVLSSAAGGKNLKSPOKVEVDIIDDNFIILNRSDSVGNVT 60  
 QY 61 FSPDYQKTMGNWIKLSCQNITSTKCNFSSIKLNVEEIKLRIRAEKENTSSWYEVDSF 120  
 Db 61 FSPDYQKTMGNWIKLSCQNITSTKCNFSSIKLNVEEIKLRIRAEKENTSSWYEVDSF 120  
 QY 121 TPFRAQIIGPPEVHLEAEDKAIVIHISPGTKDSVNMWALDGLSFTYSLLIWKNSSGVEERI 180  
 Db 121 TPFRAQIIGPPEVHLEAEDKAIVIHISPGTKDSVNMWALDGLSFTYSLLIWKNSSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
 Db 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
 QY 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 Db 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 QY 361 VTQDYPLIYEIIFWNTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARHTMDEKLNKSSV 420  
 Db 361 VTQDYPLIYEIIFWNTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARHTMDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 9

AAR42635  
 ID AAR42635 standard; protein; 557 AA.

XX AAR42635;  
 AC AAR42635;

XX 25-MAR-2003 (revised)  
 DT 20-APR-1994 (first entry)

XX Human interferon receptor.

DE IFN-R; extracellular domain; monoclonal antibody; viral infection;

KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; interferon-alpha-beta.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1. 436

FT /label= extracellular\_domain

FT /note= "soluble, immunogenic form of IFN-R"

XX EP563487-A1.

XX 06-OCT-1993.

XX 31-MAR-1992; 92EP-00400902.

XX 31-MAR-1992; 92EP-00400902.

XX (EUBI-) LAB EURO BIOTECHNOLOGIE SA.

XX Benoit P, Meyer F, Maguire D, Plavec I, Tovey MG;

XX WPI; 1993-312951/40.

DR P-PSDB; AAR42635.

PT Monoclonal antibody to human interferon type-I receptor - having

PT neutralising activity against human type I interferon, used for therapy  
PT and diagnosis.  
PS Disclosure; Fig 3; 21pp; English.  
CC Monoclonal antibodies produced against soluble forms of the human  
CC interferon alpha-beta receptor based on the full-length human IFN-R  
CC sequence are claimed. The antibodies are useful for treatment and  
CC prophylaxis of disorders involving cell proliferation and/or viral  
CC infection. (Updated on 25-MAR-2003 to correct FN field.)  
XX  
SQ Sequence 557 AA;  
  
Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
  
QY 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
Db 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
  
QY 121 TPFRKAQIGPPEVHLEAEAKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEAKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
  
QY 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPCEVNTKTCVFPQNVFQK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPCEVNTKTCVFPQNVFQK 300  
  
QY 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMDEKLNKSSV 420  
  
QY 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436  
  
RESULT 10  
ABU05091  
ID ABU05091 standard; protein; 557 AA.  
XX  
AC ABU05091;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1757.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US0095671.

XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0359895P.  
XX (ZYCO-) ZYCOS INC.  
PA Chiciz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1757; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
  
Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
  
QY 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
Db 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
  
QY 121 TPFRKAQIGPPEVHLEAEAKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEAKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
  
QY 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPCEVNTKTCVFPQNVFQK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPCEVNTKTCVFPQNVFQK 300  
  
QY 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMDEKLNKSSV 420

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QY 421 FSDAVCEKTPGNTSK 436
Db 421 FSDAVCEKTPGNTSK 436

RESULT 11
ABU05094
ID ABU05094 standard; protein; 557 AA.
AC ABU05094;
XX
XX
XX 29-JAN-2003 (first entry)
DT
DE Human expressed protein tag (EPT) #1760.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
FN
PD 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
PA
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1760; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 557 AA;
SQ

Query Match 100.0%; Score 2313; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e-199;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
cytoskeletal proteins, receptors or transcription factors), useful for
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
leukaemia.

```

PT leukemia.  
 XX Example 2; SEQ ID NO 1773; 134pp; English.  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (BPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 557 AA;  
 SQ

Query Match 100.0%; Score 2313; DB 6; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGPWLSAAGGKNLSPQKVEVDIIDNFIILRNRSDESIGNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWLSAAGGKNLSPQKVEVDIIDNFIILRNRSDESIGNVT 60

QY 61 PSFDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120  
 DB 61 PSFDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFOK 300  
 DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFOK 300

QY 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
 DB 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 360

QY 361 VTQDPLIYELIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 361 VTQDPLIYELIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420

QY 421 PSDAVCEKTKPGNTSK 436  
 DB 421 PSDAVCEKTKPGNTSK 436

RESULT 13  
 ABU05099  
 ID ABU05099 standard; protein; 557 AA.  
 XX  
 AC ABU05099;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Human expressed protein tag (BPT) #1765.  
 XX  
 KW Translational profiling; expressed protein tag (BPT); kinase; phosphatase;  
 protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 OS Homo sapiens.  
 XX WO200278524-A2.  
 PN 10-OCT-2002.  
 PD  
 XX 28-MAR-2002; 2002WO-US009671.  
 PF  
 XX 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX (ZYCO-) ZYCOS INC.  
 PA  
 XX Chicx RM, Tomlinson AJ, Urban RG;  
 XX WPI; 2003-040607/03.  
 DR  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 XX Example 2; SEQ ID NO 1765; 134pp; English.  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (BPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 557 AA;  
 SQ

Query Match 100.0%; Score 2313; DB 6; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGPWLSAAGGKNLSPQKVEVDIIDNFIILRNRSDESIGNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWLSAAGGKNLSPQKVEVDIIDNFIILRNRSDESIGNVT 60

QY 61 PSFDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120  
 DB 61 PSFDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFOK 300  
 DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFOK 300

QY 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
 DB 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 360

QY 361 VTQDPLIYELIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 361 VTQDPLIYELIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420

QY 421 PSDAVCEKTKPGNTSK 436  
 DB 421 PSDAVCEKTKPGNTSK 436

Db 241 NQNYLKWDTYNTANFTQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPFQNVFQK 300  
QY 301 GYLLRVQASDGNNTSFWESEIKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWESEIKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTPGNTSK 436  
Db 421 FSDAVCEKTPGNTSK 436

RESULT 14  
ID ABU05106 standard; protein; 557 AA.  
AC ABU05106;  
XX  
XX  
XX  
XX 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #1772.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chicz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX

New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.  
Example 2; SEQ ID NO 1772; 134pp; English.  
The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLXSPQKVEVDIIDDNFIILWRNSDESNGNT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLXSPQKVEVDIIDDNFIILWRNSDESNGNT 60  
QY 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSILKLNVEEIKLIRAEKENTSSWTEVDSF 120  
Db 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSILKLNVEEIKLIRAEKENTSSWTEVDSF 120  
QY 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
Db 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLVKQAALLTSWKIGVYSPVHCITTYENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLVKQAALLTSWKIGVYSPVHCITTYENELPPENIEVSQ 240  
QY 241 NQNYLKWDTYNTANFTQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPFQNVFQK 300  
Db 241 NQNYLKWDTYNTANFTQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPFQNVFQK 300  
QY 301 GYLLRVQASDGNNTSFWESEIKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWESEIKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTPGNTSK 436  
Db 421 FSDAVCEKTPGNTSK 436  
RESULT 15  
ID ABU05097 standard; protein; 557 AA.  
XX  
XX ABU05097;  
AC ABU05097;  
XX  
XX 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #1763.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
XX Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCOS INC.  
XX Chicz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX Example 2; SEQ ID NO 1763; 134pp; English.  
PS The invention describes a purified polypeptide, which comprises a  
PS fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAVGPMVLSAAAGGKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
Db 1 MMVLLGATTLVLVAVGPMVLSAAAGGKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 120  
Db 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 120  
QY 121 TPFRAQIGPPEVHLEAEKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRAQIGPPEVHLEAEKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
QY 181 ENIYSRHKYKLSPEYTYCLKKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKYKLSPEYTYCLKKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 NQNYLKWDTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NQNYLKWDTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GYLLRVQASDGNNTSFWEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIEBKTDVTVPNLKPLTYVCVKAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIEBKTDVTVPNLKPLTYVCVKAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTPGNTSK 436  
Db 421 FSDAVCEKTPGNTSK 436

ABU05093  
ID ABU05093 standard; protein; 557 AA.  
XX AC ABU05093;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1759.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX Example 2; SEQ ID NO 1759; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
XX fragment of a kinase, phosphatase, protease, protease inhibitor,  
XX transporter, cytoskeletal protein, receptor or transcription factor. The  
XX polypeptide is useful as an immunogenic composition for eliciting in a  
XX mammal an immunogenic response directed against any of the purified  
XX polypeptide. The purified polypeptide, or the antibody that binds to this  
XX polypeptide, is useful for treating cancer. The polypeptide is also  
XX useful for identifying compounds that binds to a naturally processed  
XX class I or class II MHC-binding polypeptide. The polypeptides and  
XX polynucleotides are particularly useful for treating or preventing  
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
XX lymphoma or leukaemia. These are also useful for screening agents for  
XX treating the above mentioned diseases. This sequence represents an  
XX expressed protein tag (EPT) isolated from human tissue for translational  
XX profiling. Note: This sequence does not appear in the printed  
XX specification but was obtained in electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAVGPMVLSAAAGGKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
Db 1 MMVLLGATTLVLVAVGPMVLSAAAGGKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNKSPQKVEVDIIDDNFILRNRSDESIGNVT 120



Db 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYBEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRAQIGPPEVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRAQIGPPEVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
QY 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Db 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 17

ABU05100  
ID ABU05100 standard; protein; 557 AA.  
XX AC ABU05100;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1766.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX FN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chicx RM, Tomlinson AJ, Urban RG;  
XX DR WPI; 2003-040607/03.  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX PS Example 2; SEQ ID NO 1766; 134pp; English.  
XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,

CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLLVAVGPVLSAAAGGKNLKSPOKVEVDIIDDNFILRWNSDESIGNVT 60  
Db 1 MMVLLGATTLLVAVGPVLSAAAGGKNLKSPOKVEVDIIDDNFILRWNSDESIGNVT 60  
QY 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYBEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYBEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRAQIGPPEVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRAQIGPPEVHLEAEDKAIVIHISPTGKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
QY 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Db 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 18

ADR66319  
ID ADR66319 standard; protein; 575 AA.  
XX AC ADR66319;  
XX DT 02-DEC-2004 (first entry)  
XX DE Human prostatic carcinoma derived protein SEQ ID 173 #2.  
XX KW human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.  
XX OS Homo sapiens.  
XX PN WO2004076614-A2.  
XX PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.  
 XX XX 27-FEB-2003; 2003DE-01009985.  
 PR PR 14-MAY-2003; 2003DE-01022134.  
 XX XX (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (ROSE/) ROSENTHAL A.  
 PA (HERM/) HERMANN K.  
 PA (PILA/) PILARSKY C.  
 XX  
 PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
 PI Xinzhang L, Staub E;  
 XX  
 DR WPI; 2004-653386/63.  
 XX  
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 XX  
 PS Claim 2; Page 653; 1607pp; German.  
 XX  
 CC This invention describes novel cytostatic polynucleotide and polypeptide  
 CC sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection  
 CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular  
 CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays,  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;  
 CC biotinylated second antibody; streptavidin-conjugated horseradish  
 CC peroxidase and then diaminobenzidine as colour former (brown). The  
 CC samples were counterstained with hemalum (blue). Malignant cells stained  
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
 CC polynucleotide and polypeptide sequences used in the method of the  
 CC invention.  
 XX  
 SQ Sequence 575 AA;  
 Query Match 100.0%; Score 2313; DB 8; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVLLGATTLVAVGPNVLSAAGKKNLSPQKVEVDIIDDNFIILNRNRSDESIGNVT 60  
 DB 19 MMVLLGATTLVAVGPNVLSAAGKKNLSPQKVEVDIIDDNFIILNRNRSDESIGNVT 78  
 QY 61 FSDYQKTMGNWIKLSCQNTSTKCNFSSKLNVYBEIKLIRAEKENTSSWEVDSE 120  
 DB 79 FSDYQKTMGNWIKLSCQNTSTKCNFSSKLNVYBEIKLIRAEKENTSSWEVDSE 138  
 QY 121 TPFRAQIQPPVHLEAEKAIIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
 DB 139 TPFRAQIQPPVHLEAEKAIIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGVEERI 198

QY 181 ENIYSRHKIYKLSPETTYCLKVKAAALTSWKIGVSPVHCIKTTVENELPPPENIEVSQ 240  
 DB 199 ENIYSRHKIYKLSPETTYCLKVKAAALTSWKIGVSPVHCIKTTVENELPPPENIEVSQ 258  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPQNVFOK 300  
 DB 259 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPQNVFOK 318  
 QY 301 GIYLLRVQASDGNNTSFWSEEEKFTEIQAFLLPPVFNIRSLSDSPHIVIGAPKQSGNTP 360  
 DB 319 GIYLLRVQASDGNNTSFWSEEEKFTEIQAFLLPPVFNIRSLSDSPHIVIGAPKQSGNTP 378  
 QY 361 VTQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 379 VTQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHTMDEKLNKSSV 438  
 QY 421 FSDAVCEKTKPGNTSK 436  
 DB 439 FSDAVCEKTKPGNTSK 454  
 RESULT 19  
 ADR66661  
 ID ADR66661 standard; protein; 575 AA.  
 AC ADR66661;  
 XX 02-DEC-2004 (first entry)  
 DT Human prostatic carcinoma derived protein SEQ ID 173 #3.  
 DE human; cytostatic; diagnosis; prostatic cancer;  
 KW differential expression analysis.  
 XX Homo sapiens.  
 OS WO2004076614-A2.  
 PN 10-SEP-2004.  
 PD 22-FEB-2004; 2004WO-DE000433.  
 PF 27-FEB-2003; 2003DE-01009985.  
 PR 14-MAY-2003; 2003DE-01022134.  
 XX (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (ROSE/) ROSENTHAL A.  
 PA (HERM/) HERMANN K.  
 PA (PILA/) PILARSKY C.  
 XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
 PI Xinzhang L, Staub E;  
 XX  
 DR WPI; 2004-653386/63.  
 XX  
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 XX  
 PS Claim 2; Page 1155; 1607pp; German.  
 XX  
 CC This invention describes novel cytostatic polynucleotide and polypeptide  
 CC sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection  
 CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular

CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.  
XX  
SQ Sequence 575 AA;

Query Match 100.0%; Score 2313; DB 8; Length 575;  
Best Local Similarity 100.0%; Pred. No. 1.1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNVLLGATTLVLVAGPWLVSAAAGGNLKSFPQVEVDIIDDNFI LRNRSDESGVNT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
19 MNVLLGATTLVLVAGPWLVSAAAGGNLKSFPQVEVDIIDDNFI LRNRSDESGVNT 78  
QY 61 FSDYQKTGMNWKLSGCQNTSTKCNFSSLKLVYBEIKLIRAEKENTSSWYEDSF 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
79 FSDYQKTGMNWKLSGCQNTSTKCNFSSLKLVYBEIKLIRAEKENTSSWYEDSF 138  
QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
139 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 198  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCITTVENELPPPEIEVSQ 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
199 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCITTVENELPPPEIEVSQ 258  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
259 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 318  
QY 301 GYLLRVQASDCGNNTSPKSEETKEPTEIQAFLLPVENIRSLSDSFHYIGAPKQSGNTP 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
319 GYLLRVQASDCGNNTSPKSEETKEPTEIQAFLLPVENIRSLSDSFHYIGAPKQSGNTP 378  
QY 361 VIQDYPLIYEIIFWNTSNAERKIEKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
379 VIQDYPLIYEIIFWNTSNAERKIEKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV 438  
QY 421 FSDAVCEKTKPGNTSK 436  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
439 FSDAVCEKTKPGNTSK 454

Search completed: January 18, 2006, 06:27:26  
Job time : 137 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:06:01 ; Search time 112.108 Seconds  
(without alignments)  
2523.620 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427  
Perfect score: 2141  
Sequence: 1 GKNLKSPQKVEVDIIDNFI.....AHTMDEKLNKSSVPSDAVCE 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05\_80:\*

1: uniprot\_sprot:\*

2: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	557	INARI_HUMAN	P17181 homo sapien
2	2141	100.0	557	Q53H11_HUMAN	Q53H11 homo sapien
3	2134	99.7	557	Q53GW9_HUMAN	Q53GW9 homo sapien
4	1912	89.3	387	Q6PKD7_HUMAN	Q6PKD7 homo sapien
5	1663.5	77.7	477	Q4R727_MACFA	Q4R727 macaca fasc
6	1438	67.2	560	INARI_PIG	Q764M8 sus scrofa
7	1384.5	64.7	560	INARI_BOVIN	Q04790 bos taurus
8	1382.5	64.6	560	INARI_SHEEP	Q28589 ovis aries
9	1082	50.5	332	Q9GK86_SHEEP	Q9GK86 ovis aries
10	966	45.1	590	INARI_MOUSE	P33896 mus musculus
11	959	44.8	590	Q8OUR8_MOUSE	Q8OUR8 mus musculus
12	958	44.7	590	Q8OUJ3_MOUSE	Q8OUJ3 mus musculus
13	677.5	31.6	449	Q5X105_CHICK	Q5X105 gallus gall
14	677.5	31.6	569	Q5XPI1_CHICK	Q5XPI1 gallus gall
15	674.5	31.5	442	Q9PVJ9_CHICK	Q9PVJ9 gallus gall
16	668.5	31.2	569	Q9VHW0_CHICK	Q9VHW0 gallus gall
17	262.5	12.3	111	Q6LD20_MOUSE	Q6LD20 mus musculus
18	246	11.5	98	Q6LD22_MOUSE	Q6LD22 mus musculus
19	229	10.7	317	Q58CP3_BOVIN	Q58CP3 bos taurus
20	220	10.3	325	Q110R2_HUMAN	Q08334 homo sapien
21	220	10.3	327	Q6ZVU9_HUMAN	Q6ZVU9 homo sapien
22	216.5	10.1	349	Q110R2_MOUSE	Q61190 mus musculus
23	216.5	10.1	351	Q8VHM7_MOUSE	Q8VHM7 mus musculus
24	202.5	9.5	362	Q764M7_PIG	Q764M7 sus scrofa
25	199	9.3	332	Q78EC1_9MURI	Q78EC1 mus sp. int
26	199	9.3	332	Q63953_MOUSE	Q63953 mus musculus
27	196	9.2	334	Q5RL90_CHICK	Q5RL90 gallus gall
28	194.5	9.1	333	Q72T30_TETNG	Q72T30 tetraodon n
29	190	8.9	59	Q9GK85_SHEEP	Q9GK85 ovis aries
30	185	8.6	213	Q8C352_MOUSE	Q8C352 mus musculus
31	183.5	8.6	341	Q9YGC8_CHICK	Q9YGC8 gallus gall

RESULT 1

ID	INARI_HUMAN	STANDARD;	PRT;	557 AA.
AC	P17181; Q8WTZ2;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-FEB-2005 (Rel. 46, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).			
GN	Name=IFNARI; Synonyms=IFNAR;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=90124632; PubMed=2153461;			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor into			
RL	mouse cells: cloning and expression of its cDNA."			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92123376; PubMed=1370833;			
RA	Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene."			
RL	J. Biol. Chem. 267:2802-2809(1992).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-168; ILE-307 AND			
RP	MET-359.			
RA	Rieder M.J., Daniele R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,			
RA	Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-			
RT	FKCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT VAL-168.			
RP	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Sange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gumarathne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

ALIGNMENTS

RA Butterfield Y.S.N., Kraywinski M.I., Skalska U., Smailus D.E.,  
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP PHOSPHORYLATION BY TYK2.  
RX MEDLINE=95059042; PubMed=7526154;  
RA Colamonici O., Yan H., Domanski P., Handa K., Smalley D.,  
RA Mullerstein J., Witte M., Krishnan K., Krolewski J.;  
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
RT of the type I interferon receptor by p135tyk2 tyrosine kinase.";  
RL Mol. Cell. Biol. 14:8133-8142(1994).  
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
CC subunits themselves.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: IFN receptors are present in all tissues and  
CC even on the surface of most IFN-resistant cells.  
CC -!- PTM: Phosphorylated on tyrosine residues by TYK2 tyrosine kinase.  
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; J03171; AA52730.1; -; mRNA.  
DR EMBL; X60459; CA42992.1; -; Genomic DNA.  
DR EMBL; AY654286; AA749100.1; -; Genomic DNA.  
DR EMBL; BC021825; AA421825.1; -; mRNA.  
DR PIR; A32694; A32694.  
DR Ensembl; ENSG00000142166; Homo sapiens.  
DR HGNC; HGNC:5432; IFNARI.  
DR H-InvDB; HIX0016075; -.  
DR MIM; 107450; -.  
DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
DR GO; GO:0004905; F: interferon-alpha/beta receptor activity; TAS.  
DR GO; GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.  
DR GO; GO:0007259; P: JAK-STAT cascade; TAS.  
DR GO; GO:0009615; P: response to virus; TAS.  
DR InterPro; IPR00282; Cytok receptor\_2.  
DR InterPro; IPR003961; FN III.  
DR PROSITE; PS00853; FN3; FALSE\_NEG.  
KW Glycoprotein; Phosphorylation; Polymorphism; Receptor; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 557 Interferon-alpha/beta receptor alpha  
FT chain.  
FT TOPO\_DOM 28 436 Extracellular (Potential).  
FT TRANSMEM 437 457 Potential.  
FT TOPO\_DOM 458 557 Cytoplasmic (Potential).  
FT DOMAIN 134 224 Fibronectin type-III 1.  
FT DOMAIN 230 326 Fibronectin type-III 2.  
FT DOMAIN 334 425 Fibronectin type-III 3.  
FT MOD\_RES 466 466 Phosphotyrosine (by TYK2) (Probable).  
FT MOD\_RES 481 481 Phosphotyrosine (by TYK2) (Probable).  
FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 81 81 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 314 314 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 416 416 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 433 433 N-linked (GlcNAc...) (Potential).  
FT DISULFID 79 87 By similarity.

FT DISULFID 199 220 By similarity.  
FT VARIANT 168 168 L -> V.  
FT /FTID=VAR\_002717.  
FT VARIANT 307 307 V -> I.  
FT /FTID=VAR\_020502.  
FT VARIANT 359 359 T -> M.  
FT /FTID=VAR\_020503.  
FT CONFLICT 17 17 A -> G (in Ref. 1).  
SQ SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75C8C CRC64;  
Query Match 100.0%; Score 2141; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 3.1e-154;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLKSPQKVEVDI IIDNFTLRNWRDSESGVNTFSDYOKTGMDNWKLSGCONITSTK 60  
DB 27 GKNLKSPQKVEVDI IIDNFTLRNWRDSESGVNTFSDYOKTGMDNWKLSGCONITSTK 86  
QY 61 CNFSSSLKLVYIEIKLRIRAEKENTSSWEVDSTFTPRKQIGPPEVHLEADKAIIVHI 120  
DB 87 CNFSSSLKLVYIEIKLRIRAEKENTSSWEVDSTFTPRKQIGPPEVHLEADKAIIVHI 146  
QY 121 SPQTKDSVMWALDGLSFTYSLIIWKNSGSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
DB 147 SPQTKDSVMWALDGLSFTYSLIIWKNSGSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206  
QY 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQONQYVLKWDYTYANMTFOVOMLHAF 240  
DB 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQONQYVLKWDYTYANMTFOVOMLHAF 266  
QY 241 KRNPNGHLYKWKQIPDCENVKTTQCVPFQNVFQGIYLLRVQASDGNNTSFWSSEIKFDT 300  
DB 267 KRNPNGHLYKWKQIPDCENVKTTQCVPFQNVFQGIYLLRVQASDGNNTSFWSSEIKFDT 326  
QY 301 EIOAFLLPPVFNIRSLSDSPHIIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIE 360  
DB 327 EIOAFLLPPVFNIRSLSDSPHIIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSADVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSADVCE 427  
RESULT 2  
Q53HL1\_HUMAN  
ID Q53HL1\_HUMAN PRELIMINARY; PRT; 557 AA.  
AC Q53HL1;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Interferon-alpha receptor 1 variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Liver;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping: a simple method to replace the cap structure of  
RT eucaryotic mRNAs with oligoribonucleotides.";  
RL Gene 138:171-174(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Liver;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;  
RT "Construction and characterization of a full length-enriched and a 5'-  
RT end-enriched cDNA library.";  
RL Gene 200:149-156(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Liver;

RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,  
RA Tanaka A., Yokoyama S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK222770; BAD96490.1; -, mRNA.  
KW Receptor.  
FT NON TER  
SQ SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75CBC CRC64;  
Query Match 100.0%; Score 2141; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 3.1e-154;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFSPDYQKTGMNDNWKLSGCCNITSTK 60  
DB 27 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFSPDYQKTGMNDNWKLSGCCNITSTK 86  
QY 61 CNFSSKLNLYVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEAEDKAIVIH 120  
DB 87 CNFSSKLNLYVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEAEDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVBERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVBERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
QY 181 LTSMKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 240  
DB 207 LTSMKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 266  
QY 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFGIYLLRVQASDGNNTSFWSEIKEDT 300  
DB 267 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFGIYLLRVQASDGNNTSFWSEIKEDT 326  
QY 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIOQYPLIYEIIFWENTSNAERKII 360  
DB 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIOQYPLIYEIIFWENTSNAERKII 386  
QY 361 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSFSDAVCE 401  
DB 387 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSFSDAVCE 427  
RESULT 3  
Q53GW9\_HUMAN PRELIMINARY; PRT; 557 AA.  
ID Q53GW9\_HUMAN PRELIMINARY; PRT; 557 AA.  
AC Q53GW9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Interferon-alpha receptor 1 variant (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping: a simple method to replace the cap structure of  
RT eucaryotic mRNAs with oligoribonucleotides.";  
RL Gene 138:171-174 (1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;  
RT "Construction and characterization of a full length-enriched and a 5'-  
RT end-enriched cDNA library.";  
RL Gene 200:149-156 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,  
RA Tanaka A., Yokoyama S.;

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK222812; BAD96532.1; -, mRNA.  
KW Receptor.  
FT NON TER  
SQ SEQUENCE 557 AA; 63598 MW; 2D9522BBCC775486 CRC64;  
Query Match 99.7%; Score 2134; DB 2; Length 557;  
Best Local Similarity 99.5%; Pred. No. 1.1e-153;  
Matches 399; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFSPDYQKTGMNDNWKLSGCCNITSTK 60  
DB 27 GKNLSPQKVEVDIIDDNFILRNWRSDESNGVTFSPDYQKTGMNDNWKLSGCCNITSTK 86  
QY 61 CNFSSKLNLYVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEAEDKAIVIH 120  
DB 87 CNFSSKLNLYVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEAEDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVBERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVBERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
QY 181 LTSMKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 240  
DB 207 LTSMKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 266  
QY 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFGIYLLRVQASDGNNTSFWSEIKEDT 300  
DB 267 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFGIYLLRVQASDGNNTSFWSEIKEDT 326  
QY 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIOQYPLIYEIIFWENTSNAERKII 360  
DB 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIOQYPLIYEIIFWENTSNAERKII 386  
QY 361 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSFSDAVCE 401  
DB 387 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSFSDAVCE 427  
RESULT 4  
Q6PKD7\_HUMAN PRELIMINARY; PRT; 387 AA.  
ID Q6PKD7\_HUMAN PRELIMINARY; PRT; 387 AA.  
AC Q6PKD7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IFNAR1 protein (Fragment).  
CN Name=IFNAR1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RA Strauberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002590; AA02590.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
FT NON TER 387  
SQ SEQUENCE 387 AA; 44388 MW; DEC1A8CC2F44499 CRC64;  
  
Query Match 89.3%; Score 1912; DB 2; Length 387;  
Best Local Similarity 99.7%; Pred. No. 5e-137;  
Matches 356; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GKNLSPQKVEVDIIDDNFILWRNSDESNGVNTFSFDYQKTGMNWKLSGCCQNIITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILWRNSDESNGVNTFSFDYQKTGMNWKLSGCCQNIITSTK 86  
  
Qy 61 CNFSSKLNVYEEIKLRIRAEKNTSSWYEVDSFTPPKKAQIGPPEVHLEAEDKAIYIHI 120  
Db 87 CNFSSKLNVYEEIKLRIRAEKNTSSWYEVDSFTPPKKAQIGPPEVHLEAEDKAIYIHI 146  
  
Qy 121 SPGTKDSVMWALDGLSFYSLIIWKNSSGVVERIENIYSRHKIYKLSPEYTYCLKVAAL 180  
Db 147 SPGTKDSVMWALDGLSFYSLIIWKNSSGVVERIENIYSRHKIYKLSPEYTYCLKVAAL 206  
  
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVOWHLAFL 240  
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVOWHLAFL 266  
  
Qy 241 KRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEIKFDT 300  
Db 267 KRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEIKFDT 326  
  
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYIIFWNTSNAERK 357  
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYIIFWNTSNAERK 383  
  
RESULT 5  
Q4R727\_MACFA  
ID Q4R727\_MACFA PRELIMINARY; PRT; 477 AA.  
AC Q4R727;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Testis cDNA, clone: QtaA-16508, similar to human interferon (alpha,  
DE beta and omega) receptor 1 (IPNARI), mRNA, RefSeq: NM\_000629.2.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopitheidae; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA International consortium for macaque cDNA sequencing, analysis;  
RT "DNA sequences of macaque genes expressed in brain or testis and its  
RL evolutionary implications";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,  
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;  
RT "Substitution rate and structural divergence of 5' UTR evolution:  
RT Comparative analysis between human and cynomolgus monkey cDNAs";  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

DR EMBL; AB169002; BAB01097.1; -; mRNA.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
KW Receptor; Transmembrane.  
SQ SEQUENCE 477 AA; 54766 MW; 1D4110D471060BCF CRC64;  
  
Query Match 77.7%; Score 1663.5; DB 2; Length 477;  
Best Local Similarity 91.1%; Pred. No. 5.3e-118;  
Matches 316; Conservative 10; Mismatches 20; Indels 1; Gaps 1;  
  
Qy 56 ITSTKCNFSSKLNVYEEIKLRIRAEKNTSSWYEVDSFTPPKKAQIGPPEVHLEAEDKA 115  
Db 1 MTSTKCNFSSKLNVYEEIKLRIRAEKNTSSWYEVDSFTPPKKAQIGPPEVHLEAEDKA 60  
  
Qy 116 IVIHIS-PGTKDSVMWALDGLSFYSLIIWKNSSGVVERIENIYSRHKIYKLSPEYTYCL 174  
Db 61 IVIYISPPGTTSDSVMMALDRSSFTYSLIWKNSGVVERIENIYSRHKIYKLSPEYTYCL 120  
  
Qy 175 KVKAALLTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVQ 234  
Db 121 KVKAALLTSRKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVQ 180  
  
Qy 235 WLHAFILKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSE 294  
Db 181 WLHAFILKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSE 240  
  
Qy 295 EIKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYIIFWNTSNA 354  
Db 241 EIKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYIIFWNTSNA 300  
  
Qy 355 ERKIIKKKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSVFSFVAVCE 401  
Db 301 ERKIIKKKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSVFSFVAVCE 347  
  
RESULT 6  
INARI\_PIG  
ID INARI\_PIG STANDARD; PRT; 560 AA.  
AC Q764M6;  
DT 10-MAY-2005 (Rel. 47, Created)  
DT 10-MAY-2005 (Rel. 47, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
GN Name=IFNARI;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX PubMed=14681463; DOI=10.1093/nar/gkh037;  
RA Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,  
RA Okumura N., Hamasima N., Awata T.;  
RT "PEDE (Pig EST Data Explorer): construction of a database for ESTs  
RT derived from porcine full-length cDNA libraries.";  
RL Nucleic Acids Res. 32:D484-D488(2004).  
CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
CC subunits themselves (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; AB116561; BAD06315.1; -; mRNA.  
DR InterPro; IPR000282; Cytok\_receptor\_2.  
DR InterPro; IPR003961; FN\_III.



DR PROSITE, PS50853; FN3; FALSE\_NEG.  
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.  
 FT TOPO\_DOM 25 437 Extracellular (Potential).  
 FT TRANSMEM 438 458 Potential.  
 FT TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 FT DOMAIN 133 224 Fibronectin type-III 1.  
 FT DOMAIN 230 326 Fibronectin type-III 2.  
 FT DOMAIN 334 426 Fibronectin type-III 3.  
 FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 222 222 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 SQ SEQUENCE 560 AA; 63221 MW; DC193651033DFBDB CRC64;

Query Match 67.2%; Score 1438; DB 1; Length 560;  
 Best Local Similarity 66.4%; Pred. No. 9.3e-101;  
 Matches 269; Conservative 63; Mismatches 69; Indels 4; Gaps 4;

QY 1 GNKLSPKQVEVDIIDDNFILRWNSDRSGVNTFSFDYQKGMNDWLKSGCNITSTK 60  
 DB 24 GADLRSPENVVSIIDDFILRWNSDRSGVNTFSADYQITGMNDWLKPGCQVSTSE 83  
 QY 61 CNFSSKLK-NVYEIKLIRAEKEN-TSSWYVDSTFPRKAQIGPPEVHLEAEDKAIVI 118  
 DB 84 CNFSSIKLVYEKTKLIRAEKNGSTSPWYEVFPFQEAQIGPDPVHLEAEDKAI 143  
 QY 119 HIS-PGTQKDSVMWALDGLSFTYSLLIWNKSGVEERIENIYSRHKYIKLSPETTYCLKVK 177  
 DB 144 NLSPPGTQKDSVMWAMDSSFFVSLVWKNSSLEERTKTVDARDKHQLSPETTYCLKVK 203  
 QY 178 AALLTSWIKGVSPVHCITVTENELPPENLEVSQNVQNYLKWDTYVNTTFOVWLH 237  
 DB 204 AGLRSPKGVSPVSPYICITNTTKHLLPSPENLEINAEVNVYLVKNYTYENTTFOVWLH 263  
 QY 238 AFLKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSPWSEIK 297  
 DB 264 AFLKKIPEDHSDKWKQIPCNENKTHCVFPQNVTKGIFFIRVQASNGNSTSLSEKR 323  
 QY 298 FDTETQAFLLPVPFNIRSLSD-SFHYIYCAPKQSGNTPTVIDYPLIYIIFWENTSNAER 356  
 DB 324 FNTENQTLFPVPVINKPINDASLRVGIGAPKESDKSVNQLYPLIYEVIPRENTSDTER 383  
 QY 357 KLIKKTDTVPLNPLTYCVKARAHWTDEKLNKSSVPSFDACE 401  
 DB 384 DVLEKRTDTFTSNLPLTYCVKARALIENDRWNRSSVPSFDVCE 428

## RESULT 7

INARI\_BOVIN STANDARD; PRT; 560 AA.  
 ID INARI\_BOVIN  
 AC Q04790;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
 GN Name=IFNARI; Synonyms=IFNAR;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=93076908; PubMed=1446745; DOI=10.1016/0014-5793(92)81204-Y;  
 RA "Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;  
 RT "Specific antiviral activities of the human alpha interferons are  
 RL determined at the level of receptor (IFNAR) structure.";  
 RL FEBS Lett. 313:255-259(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93305725; PubMed=8318540; DOI=10.1016/0167-4781(93)90129-2;  
 RA Lim J.-K., Langer J.A.;  
 RL "Cloning and characterization of a bovine alpha interferon receptor.";  
 RL Biochim. Biophys. Acta 1173:314-319(1993).  
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
 CC including JAKs, TYK2, STAT proteins and IFNAR alpha- and beta-  
 CC subunits themselves.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; X68443; CAA48484.1; -; mRNA.  
 DR EMBL; L06320; AAA02571.1; -; mRNA.  
 DR PIR; S27387; S27387.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001187; Tissue\_factor.  
 DR Pfam; PF01108; Tissue\_fac; 1.  
 DR PROSITE; PS50853; FN3; 2.  
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.  
 FT TOPO\_DOM 25 437 Extracellular (Potential).  
 FT TRANSMEM 438 458 Potential.  
 FT TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 FT DOMAIN 133 224 Fibronectin type-III 1.  
 FT DOMAIN 230 326 Fibronectin type-III 2.  
 FT DOMAIN 334 426 Fibronectin type-III 3.  
 FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 FT CONFLICT 422 422 F -> V (in Ref. 2).  
 SQ SEQUENCE 560 AA; 63819 MW; 66D76B72861B1D11 CRC64;

Query Match 64.7%; Score 1384.5; DB 1; Length 560;  
 Best Local Similarity 64.0%; Pred. No. 1.1e-96;  
 Matches 258; Conservative 62; Mismatches 78; Indels 5; Gaps 5;

QY 3 NLKSPQKVEVDIIDDNFILRWNSDRSGVNTFSFDYQKGMNDWLKSGCNITSTKCN 62  
 DB 27 NLK-PENVEIHIDDFILRWNSDRSGVNTFSADYQITGMNDWLKSGCNITSTKCN 85  
 QY 63 FSSKLK-NVYEIKLIRAEKEN-TSSWYVDSTFPRKAQIGPPEVHLEAEDKAIVI 120  
 DB 86 FSSVELENVFEKILIRAEKNGNTSTWYEVFPFQEAQIGPDPVHLEAEDKAI 145  
 QY 121 S-PGTQKDSVMWALDGLSFTYSLLIWNKSGVEERIENIYSRHKYIKLSPETTYCLKVKAA 179

Db 146 SPPTGDSIMWMDRSSFRYSVWIKNSSSLEERTETVYPBCKIYKLSPEITTYCLKVKAE 205  
 Qy 180 LLTSWKIGVSPVHCITKTVENELPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 239  
 Db 206 LRQSRVGCYSPVCINTTERHKVPSQINADNQIYVLKWDYTYANMTFQVQWLHAF 265  
 Qy 240 LKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEEEKFD 299  
 Db 266 FKIPGNHSDKWKQIPNCENVTSTHCVFPREVSSRGYVVRASNGNGTSFWSEEEKFN 325  
 Qy 300 TEIQAFLLPPVFNIRSL-DSFHYIYGAPKQSGNTVPIQDYPLIYEIIFWENTSNAERKI 358  
 Db 326 TEMKTIIPFPVISMKSITDLSHVSASESESNMNSQYLYPLIYEIIFWENTSNAERKV 385  
 Qy 359 IEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVPSDAVCE 401  
 Db 386 LEKRTDFTFENLAPLTVYCVKARALIENTDRNKGSSSDTVCE 428

RESULT 8  
 INARI SHEEP  
 ID INARI1 SHEEP STANDARD; PRT; 560 AA.  
 AC Q28585; Q95206;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)  
 DE (Interferon alpha/beta receptor-1).  
 GN Name=IFNAR1; Synonyms=IFNAR;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Endometrium;  
 RX MEDLINE=97135690; PubMed=8981227; DOI=10.1677/jme.0.0170207;  
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;  
 RT "Structure of an ovine interferon receptor and its expression in  
 endometrium.";  
 RL J. Mol. Endocrinol. 17:207-215 (1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Endometrium;  
 RX MEDLINE=98008426; PubMed=9348203; DOI=10.1210/en.138.11.4757;  
 RA Han C.-S., Mathaiagan N., Klemann S.W., Roberts R.M.;  
 RT "Molecular cloning of ovine and bovine type I interferon receptor  
 subunits from uteri, and endometrial expression of messenger  
 ribonucleic acid for ovine receptors during the estrous cycle and  
 pregnancy.";  
 RL Endocrinology 138:4757-4767 (1997).  
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
 CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
 CC subunits themselves.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined except  
 CC conceptus at day 15 of pregnancy.  
 CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X95939; CAA65183.1; -; mRNA.  
 CC EMBL; U65978; AAB84231.1; -; mRNA.  
 CC InterPro; IPR000282; Cytok\_receptor\_2.  
 CC InterPro; IPR003961; FN\_III.  
 CC PROSITE; PS50853; FN3; 3.

KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24 By similarity.  
 FT FT 25 560 Interferon-alpha/beta receptor alpha  
 FT chain.  
 FT FT Extracellular (Potential).  
 FT TOPO\_DOM 25 437 Potential.  
 FT TRANSMEM 438 458  
 FT TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 FT DOMAIN 125 224 Fibronectin type-III 1.  
 FT DOMAIN 230 326 Fibronectin type-III 2.  
 FT DOMAIN 330 426 Fibronectin type-III 3.  
 FT CARBOHYD 47 47 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 55 55 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 85 85 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 108 108 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 109 109 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 172 172 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 222 222 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 285 285 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 313 313 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 359 359 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 377 377 N-linked (GLCNAC. .) (Potential).  
 FT CARBOHYD 434 434 N-linked (GLCNAC. .) (Potential).  
 FT DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 FT CONFLICT 352 352 S -> G (in Ref. 2).  
 FT CONFLICT 522 522 A -> D (in Ref. 2).  
 SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

Query Match 64.8%; Score 1382.5; DB 1; Length 560;  
 Best Local Similarity 63.5%; Pred. No. 1.5e-96;  
 Matches 256; Conservative 65; Mismatches 77; Indels 5; Gaps 5;

Qy 3 NLKSPQKVEVDIIDDNFILRWNSDSEGVNVTFSFYQKGTGMWNWIKLSCQNITTSKCN 62  
 Db 27 NLKS-ENVEIHIIDDNFFLKNSSSVNRVTSADYQILGTDNWKKLPGCHITSSKN 85  
 Qy 63 FSSIKL-NVYEEIKLRIRAEK-ENTSSWYEVDSFTPRKQAIQGPPEVHLAEADKAIYIHI 120  
 Db 86 FSSVELKQVFEKIELIRAEENNTSTWYEVFPFLKQAIQGPDPVHLEADKAIILSI 145  
 Qy 121 S-PGTQDSVMWALDGLSFTYSLIWNKSSGVBERIENIYSRHKIYKLSPEITTYCLKVAA 179  
 Db 146 SPFGTDSIMWALDRSSFRYSVWIKNSSSLEERTETVYPBCKIYKLSPEITTYCLKVAAE 205  
 Qy 180 LLTSWKIGVSPVHCITKTVENELPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 239  
 Db 206 LRQSRVGCYSPVCINTTERHKVPSQINADNQIYVLKWDYTYANMTFQVQWLHAF 265  
 Qy 240 LKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEEEKFD 299  
 Db 266 LKXIPGKSNKQIIPNCENVTSTHCVFPREVSSRGYVVRASNGNGTSFWSEEEKFN 325  
 Qy 300 TEIQAFLLPPVFNIRSL-DSFHYIYGAPKQSGNTVPIQDYPLIYEIIFWENTSNAERKI 358  
 Db 326 TEVKPIIFPPVISMKSITDLSHVSASESESNMNSQYLYPLIYEIIFWENTSNAERKV 385  
 Qy 359 IEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVPSDAVCE 401  
 Db 386 LEKRTDFTFENLAPLTVYCVKARALIENTDRNKGSSSDTVCE 428

RESULT 9  
 Q9GK86 SHEEP  
 ID Q9GK86 SHEEP PRELIMINARY; PRT; 332 AA.  
 AC Q9GK86;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Type I interferon receptor 1e.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.







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Db 90 HTECDFSSAITAYDYTHIRAEERREAKSPWSSIPFEMIPYEIAQIGPPEIALQSGINGAI 149
Qy 117 VIHISPTKDSV--MWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPEPTYCL 174
Db 150 KINISPPKANQVRKMW-LISVFFKYNVIVDNNSSNV-EKVRSLIPDIDVINDLAPETTYCL 207
Qy 175 KVAALTLTSWKIGVSPVHCIKTTVE--NELPPPENIEVSVQNONYVLKWDYTY--ANMTFQ 232
Db 208 KVQATVPLEDKGLFSPHICIKITRKVNDLLCPTNVRVFAFNKMFYLLWNNHNEHYTYT 267
Qy 233 VQWLHAPLKRNPNGNHLKWKQIPDCENVKTTQC-----VFPQNVFQKGIYLLRVQASDGN 287
Db 268 VQYLTGVLKLNLYDDYSKWKQKVSVCENITSMKCNLSGVIKPTS----ASYVFRVQAMNEY 323
Qy 288 NTSFMSSEIKFDPTEIOAFLLPPVFNIRSLSDSHIYIGAPKQSGNTPTVIQDYLPIYELIF 347
Db 324 NKSLSKDVEVDPVVTNEIGPPDVKDIDSVLLHIIKITPPGPGNKMISLDLYDFPYQILY 383
Qy 348 WENTSNAERKIIIEKKTID---VTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVC 400
Db 384 WKSSDNEEBEVKMKETKQTIATVSDLPASTLYCVKQVA--FSEAYNKSSDFSREEC 437
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RESULT 15

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Q9PVJ9_CHICK
ID Q9PVJ9 CHICK PRELIMINARY; PRT; 442 AA.
AC Q9PVJ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Interferon alpha/beta receptor 1 (Fragment).
GN Name=IFNAR1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR ENBL; AF082667; AAD13679.1; -; Genomic DNA.
DR Ensembl; ENSGALG0000015942; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PSS0853; FN3; 4.
KW Receptor.
FT NON TER
SQ SEQUENCE 442 442 49877 MW; 839EBE92170609E0 CRC64;
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Query Match 31.5%; Score 674.5; DB 2; Length 442;
Best Local Similarity 38.2%; Pred. No. 8.1e-43;
Matches 159; Conservative 76; Mismatches 154; Indels 27; Gaps 12;

Qy 3 NLKSPQKVEVDIIDDNFILRWNSDSGVNVTFSFDYQ----KTGMDNWKLSGCONIT 57
Db 31 NLKSPQDIQYAVNTFLWNYTGDGT-NVTFSAQYQCFDDLDQTSPEWKELSGCONVS 89
Qy 58 STKCNFSSKLINVEYIKLIRAF-KENTSSWEVDSFTPFKAQIGPPEVHLEAEDKAI 116
Db 90 HTECDFSSAITAYDYTHIRAEERREAKSPWSSIPFEMIPYEIAQIGPPEIALQSGINGAI 149
Qy 117 VIHISPTKDSV--MWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPEPTYCL 174
Db 150 KINISPPKANQVRKMW-LISVFFKYNVIVDNNSSNV-EKVRSLIPDIDVINDLAPETTYCL 207
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Qy 175 KVAALTLTSWKIGVSPVHCIKTTVE--NELPPPENIEVSVQNONYVLKWDYTY--ANMTFQ 232
Db 208 KVQATVPLEDKGLFSPHICIKITRKVNDLLCPTNVRVFAFNKMFYLLWNNHNEHYTYT 267
Qy 233 VQWLHAPLKRNPNGNHLKWKQIPDCENVKTTQC-----VFPQNVFQKGIYLLRVQASDGN 287
Db 268 VQYLTGVLKLNLYDDYSKWKQKVSVCENITSMKCNLSGVIKPTS----ASYVFRVQAMNEY 323
Qy 288 NTSFMSSEIKFDPTEIOAFLLPPVFNIRSLSDSHIYIGAPKQSGNTPTVIQDYLPIYELIF 347
Db 324 NKSLSKDVEVDPVVTNEIGPPDVKDIDSVLLHIIKITPPGPGNKMISLDLYDFSYQILY 383
Qy 348 WENTSNAERKIIIEKKTID---VTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVC 400
Db 384 WKSSDNEEBEVKMKETKQTIATVSDLPASTLYCVKQVA--FSEAYNKSSDFSREEC 437
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Search completed: January 17, 2006, 07:18:43  
Job time : 113.108 secs